SEQUENCE LISTING

<110> Chang, Chawnshang

<120> Androgen Receptor Coregulators

<130> 21108.0011U6

<140> 10/517,155
<141> 2005-01-06

<150> PCT/US03/17937
<151> 2003-06-06

<150> US 60/387,087
<151> 2002-06-06

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<170> FastSEQ for Windows Version 4.0

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<213> Homo sapien

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      C-terminal domain

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<223> Coding sequence and polypeptide region which may
      form a cystein-rich RING finger motif

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<223> Coding sequence and polypeptide region for a
      cystein-rich B box like structure

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                                            Met Ser Ser Glu Asp
                                             1   5

cga gaa gct cag gag gat gaa ttg ctg gcc ctg gca agt att tac gat   102
Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp
               10   15   20

1

```
gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg      150
Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg
            25                  30                  35

atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat      198
Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn
            40                  45                  50

tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt      246
Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe
        55                  60                  65

ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc      294
Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser
70                  75                  80                  85

tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act      342
Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr
                90                  95                  100

cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac      390
Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His
            105                 110                 115

cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag      438
Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu
            120                 125                 130

acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt      486
Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly
        135                 140                 145

tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca      534
Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr
150                 155                 160                 165

gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa      582
Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu
                170                 175                 180

att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg      630
Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu
            185                 190                 195

atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt      678
Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe
            200                 205                 210

aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt      726
Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly
        215                 220                 225

agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc      774
Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala
230                 235                 240                 245

tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa      822
Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln
            250                 255                 260
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tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt       870
Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly
            265             270             275

cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc       918
Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg
            280             285             290

ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc       966
Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys
            295             300             305

ccc cgg ccg tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc      1014
Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr
310             315             320             325

atg ggt atc tgc tcc agc tgc aat ttt gcc ttc tgt act ttg tgc agg      1062
Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg
            330             335             340

ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta      1110
Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val Thr Ala Glu Lys Leu
            345             350             355

atg gac tta cga aat gaa tac ctg caa gcg gat gag gct aat aaa aga      1158
Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp Glu Ala Asn Lys Arg
            360             365             370

ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa      1206
Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu
            375             380             385

gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca      1254
Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro
390             395             400             405

tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca      1302
Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr
            410             415             420

tgt act ggc tgt atg caa tat ttc tgt tgg att tgc atg ggt tct ctc      1350
Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu
            425             430             435

tct aga gca aac cct tac aaa cat ttc aat gac cct ggt tca cca tgt      1398
Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys
            440             445             450

ttt aac cgg ctg ttt tat gct gtg gat gtt gac gac gat att tgg gaa      1446
Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp Asp Asp Ile Trp Glu
            455             460             465

gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg            1494
Asp Glu Val Glu Asp *
470


ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt    1554
tgcgggatat ttagggtact attcattcac tcttcctgcg tagaagatat ggaagaacga    1614
ggtttatatt ttcatgtggt actactgaag aaggtgcatt gatacatttt taaatgtaag    1674
ttgagaaaaa tttataagcc aaaggttcag aaaattaaac tacagaa                  1721
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<210> 2
<211> 474
<212> PRT
<213> Homo sapien

<400> 2

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Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
 1               5                  10                  15
Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
                20                  25                  30
Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
        35                  40                  45
Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
    50                  55                  60
Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
65                  70                  75                  80
Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
                85                  90                  95
Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
                100                 105                 110
Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
        115                 120                 125
Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe
    130                 135                 140
Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln
145                 150                 155                 160
Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp
                165                 170                 175
Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu
                180                 185                 190
Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln
        195                 200                 205
Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe
    210                 215                 220
Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His
225                 230                 235                 240
Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg
                245                 250                 255
Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser
                260                 265                 270
Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe
        275                 280                 285
Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala
    290                 295                 300
Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln
305                 310                 315                 320
Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe
                325                 330                 335
Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val
                340                 345                 350
Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp
        355                 360                 365
Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile
    370                 375                 380
Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn
385                 390                 395                 400
Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly
                405                 410                 415
Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile
                420                 425                 430
```

4

```
Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
        435             440             445
Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
    450             455             460
Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
465             470
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<210> 3
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<213> Homo sapien

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<222> (631)...(783)
<223> Coding sequence and polypeptide region for a
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<221> misc_feature
<222> (808)...(996)
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<220>
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<220>
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atg cca agg tca ggg gct ccc aaa gag cgc cct gcg gag cct ctc acc    48
Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
 1               5               10              15

cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct    96
Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
            20              25              30

tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag   144
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
            35              40              45
```

```
cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct          192
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
        50              55                  60

tcc agc ggt gtc ttg ggt acc ggg ctc tgt gag cta gat cgg ttg ctt          240
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
65                  70                  75                  80

cag gaa ctt aat gcc act cag ttc aac atc aca gat gaa atc atg tct          288
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
                    85                  90                  95

cag ttc cca tct agc aag gtg gct tca gga gag cag aag gag gac cag          336
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
            100                 105                 110

tct gaa gat aag aaa aga ccc agc ctc cct tcc agc ccg tct cct ggc          384
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
            115                 120                 125

ctc cca aag gct tct gcc acc tca gcc act ctg gag ctg gat aga ctg          432
Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
        130                 135                 140

atg gcc tca ctc cct gac ttc cgc gtt caa aac cat ctt cca gcc tct          480
Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145                 150                 155                 160

ggg cca act cag cca ccg gtg gtg agc tcc aca aat gag ggc tcc cca          528
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
                    165                 170                 175

tcc cca cca gag ccg act gca aag ggc agc cta gac acc atg ctg ggg          576
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
            180                 185                 190

ctg ctg cag tcc gac ctc agc cgc cgg ggt gtt ccc acc cag gcc aaa          624
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
        195                 200                 205

ggc ctc tgt ggc tcc tgc aat aaa cct att gct ggg caa gtg gtg acg          672
Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
        210                 215                 220

gct ctg ggc cgc gcc tgg cac ccc gag cac ttc gtt tgc gga ggc tgt          720
Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225                 230                 235                 240

tcc acc gcc ctg gga ggc agc agc ttc ttc gag aag gat gga gcc ccc          768
Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
                    245                 250                 255

ttc tgc ccc gag tgc tac ttt gag cgc ttc tcg cca aga tgt ggc ttc          816
Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
            260                 265                 270

tgc aac cag ccc atc cga cac aag atg gtg acc gcc ttg ggc act cac          864
Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
            275                 280                 285
```

6

```
tgg cac cca gag cat ttc tgc tgc gtc agt tgc ggg gag ccc ttc gga          912
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
    290                     295                 300

gat gag ggt ttc cac gag cgc gag ggc cgc ccc tac tgc cgc cgg gac          960
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305                     310                 315                 320

ttc ctg cag ctg ttc gcc ccg cgc tgc cag ggc tgc cag ggc ccc atc         1008
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
                325                 330                 335

ctg gat aac tac atc tcg gcg ctc agc ctg ctc tgg cac ccg gac tgt         1056
Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys
                340                 345                 350

ttc gtc tgc agg gaa tgc ttc gcg ccc ttc tcg gga ggc agc ttt ttc         1104
Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe
            355                 360                 365

gag cac gag ggc cgc ccg ttg tgc gag aac cac ttc cac gca cga cgc         1152
Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg
    370                 375                 380

ggc tcg ctg tgc ccc acg tgt ggc ctc cct gtg acc ggc cgc tgc gtg         1200
Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val
385                 390                 395                 400

tcg gcc ctg ggt cgc cgc ttc cac ccg gac cac ttc gca tgc acc ttc         1248
Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe
                405                 410                 415

tgc ctg cgc ccg ctc acc aag ggg tcc ttc cag gag cgc gcc ggc aag         1296
Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys
                420                 425                 430

ccc tac tgc cag ccc tgc ttc ctg aag ctc ttc ggc tga                     1335
Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly
            435                 440
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<210> 4
<211> 444
<212> PRT
<213> Homo sapien

<400> 4

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Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
 1               5                   10                  15
Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
                20                  25                  30
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
            35                  40                  45
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
    50                  55                  60
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
65                  70                  75                  80
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
                85                  90                  95
```

7

```
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
            100             105             110
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
            115             120             125
Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
            130             135             140
Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145             150             155             160
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
            165             170             175
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
            180             185             190
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
            195             200             205
Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
            210             215             220
Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225             230             235             240
Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
            245             250             255
Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
            260             265             270
Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
            275             280             285
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
            290             295             300
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305             310             315             320
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
            325             330             335
Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys
            340             345             350
Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe
            355             360             365
Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg
            370             375             380
Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val
385             390             395             400
Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe
            405             410             415
Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys
            420             425             430
Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly
            435             440
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<211> 1566
<212> DNA
<213> Homo sapien

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<222> (676)...(1566)

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<221> 5'UTR
<222> (1)...(24)
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8

<400> 5

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ggcgcttctg gaaggaacgc cgcg atg gct gcg cag gga gag ccc cag gtc        51
                           Met Ala Ala Gln Gly Glu Pro Gln Val
                           1                   5


cag ttc aaa ctt gta ttg gtt ggt gat ggt ggt act gga aaa acg acc     99
Gln Phe Lys Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr
 10              15                  20                  25


ttc gtg aaa cgt cat ttg act ggt gaa ttt gag aag aag tat gta gcc    147
Phe Val Lys Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala
                30                  35                  40


acc ttg ggt gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga    195
Thr Leu Gly Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly
                45                  50                  55


cct att aag ttc aat gta tgg gac aca gcc ggc cag gag aaa ttc ggt    243
Pro Ile Lys Phe Asn Val Trp Asp Thr Ala Gly Gln Glu Lys Phe Gly
            60                  65                  70


gga ctg aga gat ggc tat tat atc caa gcc cag tgt gcc atc ata atg    291
Gly Leu Arg Asp Gly Tyr Tyr Ile Gln Ala Gln Cys Ala Ile Ile Met
        75                  80                  85


ttt gat gta aca tcg aga gtt act tac aag aat gtg cct aac tgg cat    339
Phe Asp Val Thr Ser Arg Val Thr Tyr Lys Asn Val Pro Asn Trp His
 90                  95                  100                 105


aga gat ctg gta cga gtg tgt gaa aac atc ccc att gtg ttg tgt ggc    387
Arg Asp Leu Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly
                110                 115                 120


aac aaa gtg gat att aag gac agg aaa gtg aag gcg aaa tcc att gtc    435
Asn Lys Val Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val
                125                 130                 135


ttc cac cga aag aag aat ctt cag tac tac gac att tct gcc aaa agt    483
Phe His Arg Lys Lys Asn Leu Gln Tyr Tyr Asp Ile Ser Ala Lys Ser
            140                 145                 150


aac tac aac ttt gaa aag ccc ttc ctc tgg ctt gct agg aag ctc att    531
Asn Tyr Asn Phe Glu Lys Pro Phe Leu Trp Leu Ala Arg Lys Leu Ile
    155                 160                 165


gga gac cct aac ttg gaa ttt gtt gcc atg cct gct ctc gcc cca cca    579
Gly Asp Pro Asn Leu Glu Phe Val Ala Met Pro Ala Leu Ala Pro Pro
170                 175                 180                 185


gaa gtt gtc atg gac cca gct ttg gca gca cag tat gag cac gac tta    627
Glu Val Val Met Asp Pro Ala Leu Ala Ala Gln Tyr Glu His Asp Leu
                190                 195                 200


gag gtt gct cag aca act gct ctc ccg gat gag gat gat gac ctg tga    675
Glu Val Ala Gln Thr Thr Ala Leu Pro Asp Glu Asp Asp Asp Leu
                205                 210                 215


gaatgaagct ggagcccagc gtcagaagtc tagttttata ggcagctgtc ctgtgatgtc    735
agcggtgcag cgtgtgtgcc acctcattat tatctagcta agcggaacat gtgctttatc    795
tgtgggatgc tgaaggagat gagtgggctt cggagtgaat gtggcagttt aaaaaataac    855
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ttcattgttt ggacctgcat atttagctgt ttggacgcag ttgattcctt gagtttcata    915
tataagactg ctgcagtcac atcacaatat tcagtggtga aatcttgttt gttactgtca    975
ttcccattcc ttttctttag aatcagaata aagttgtatt tcaaatatct aagcaagtga   1035
actcatccct tgtttataaa tagcatttgg aaaccactaa agtagggaag ttttatgcca   1095
tgttaatatt tgaattgcct tgcttttatc acttaatttg aaatctattg ggttaatttc   1155

tccctatgtt tattttttgta catttgagcc atgtcacaca aactgatgat gacaggtcag   1215
cagtattcta tttggttaga agggttacat ggtgtaaata ttagtgcagt taagctaaag   1275
cagtgtttgc tccaccttca tattggctag gtagggtcac ctagggaagc acttgctcaa   1335
aatctgtgac ctgtcagaat aaaaatgtgg tttgtacata tcaaatagat attttaaggg   1395
taatattttc ttttatggca aaagtaatca tgttttaatg tagaacctca aacaggatgg   1455
aacatcagtg gatggcagga ggttgggaat tcttgctgtt aaaaataatt acaaattttg   1515
cactttttgt ttgaatgtta gatgcttagt gtgaagttga tacgcaagcc g           1566
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<210> 6
<211> 216
<212> PRT
<213> Homo sapien

<400> 6

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Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
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Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
            20                  25                  30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
        35                  40                  45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
    50                  55                  60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65                  70                  75                  80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
            85                  90                  95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
            100                 105                 110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
            115                 120                 125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
    130                 135                 140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145                 150                 155                 160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
                165                 170                 175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
                180                 185                 190
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
        195                 200                 205
Leu Pro Asp Glu Asp Asp Asp Leu
    210                 215
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<210> 7
<211> 4839
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (138)...(2924)

<400> 7

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gcgtgccccg cgtgcgcgcg cgtcgtcctc cccggcgctc ctccacagct cgctggctcc   120
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cgccgcggaa aggcgtc atg ccg ccc aaa acc ccc cga aaa acg gcc gcc         170
                    Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
                     1               5                  10

acc gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc         218
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
            15                  20                  25

cct cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct         266
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
            30                  35                  40

ctc gtc agg ctt gag ttt gaa gaa aca gaa gaa cct gat ttt act gca         314
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
        45                  50                  55

tta tgt cag aaa tta aag ata cca gat cat gtc aga gag aga gct tgg         362
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60                  65                  70                  75

tta act tgg gag aaa gtt tca tct gtg gat gga gta ttg gga ggt tat         410
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
                80                  85                  90

att caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca gca         458
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
            95                  100                 105

gtt gac cta gat gag atg tcg ttc act ttt act gag cta cag aaa aac         506
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
            110                 115                 120

ata gaa atc agt gtc cat aaa ttc ttt aac tta cta aaa gaa att gat         554
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
        125                 130                 135

acc agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat         602
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
140                 145                 150                 155

gat gta ttg ttt gca ctc ttc agc aaa ttg gaa agg aca tgt gaa ctt         650
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
            160                 165                 170

ata tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct         698
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
            175                 180                 185

gca ttg gtg cta aaa gtt tct tgg atc aca ttt tta tta gct aaa ggg         746
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
            190                 195                 200

gaa gta tta caa atg gaa gat gat ctg gtg att tca ttt cag tta atg         794
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
        205                 210                 215

cta tgt gtc ctt gac tat ttt att aaa ctc tca cct ccc atg ttg ctc         842
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
220                 225                 230                 235
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aaa gaa cca tat aaa aca gct gtt ata ccc att aat ggt tca cct cga    890
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
            240                 245                 250

aca ccc agg cga ggt cag aac agg agt gca cgg ata gca aaa caa cta    938
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
            255                 260                 265

gaa aat gat aca aga att att gaa gtt ctc tgt aaa gaa cat gaa tgt    986
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
            270                 275                 280

aat ata gat gag gtg aaa aat gtt tat ttc aaa aat ttt ata cct ttt   1034

Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
            285                 290                 295

atg aat tct ctt gga ctt gta aca tct aat gga ctt cca gag gtt gaa   1082
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu

300                 305                 310                 315

aat ctt tct aaa cga tac gaa gaa att tat ctt aaa aat aaa gat cta   1130
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
                320                 325                 330

gat gca aga tta ttt ttg gat cat gat aaa act ctt cag act gat tct   1178
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
            335                 340                 345

ata gac agt ttt gaa aca cag aga aca cca cga aaa agt aac ctt gat   1226
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
            350                 355                 360

gaa gag gtg aat gta att cct cca cac act cca gtt agg act gtt atg   1274
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
            365                 370                 375

aac act atc caa caa tta atg atg att tta aat tca gca agt gat caa   1322
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
380                 385                 390                 395

cct tca gaa aat ctg att tcc tat ttt aac aac tgc aca gtg aat cca   1370
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
            400                 405                 410

aaa gaa agt ata ctg aaa aga gtg aag gat ata gga tac atc ttt aaa   1418
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
            415                 420                 425

gag aaa ttt gct aaa gct gtg gga cag ggt tgt gtc gaa att gga tca   1466
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser
            430                 435                 440

cag cga tac aaa ctt gga gtt cgc ttg tat tac cga gta atg gaa tcc   1514
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
            445                 450                 455

atg ctt aaa tca gaa gaa gaa cga tta tcc att caa aat ttt agc aaa   1562
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
460                 465                 470                 475
```

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ctt ctg aat gac aac att ttt cat atg tct tta ttg gcg tgc gct ctt    1610
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
            480             485                 490

gag gtt gta atg gcc aca tat agc aga agt aca tct cag aat ctt gat    1658
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp
            495             500                 505

tct gga aca gat ttg tct ttc cca tgg att ctg aat gtg ctt aat tta    1706
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
            510             515                 520

aaa gcc ttt gat ttt tac aaa gtg atc gaa agt ttt atc aaa gca gaa    1754
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
            525             530                 535

ggc aac ttg aca aga gaa atg ata aaa cat tta gaa cga tgt gaa cat    1802
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
540             545                 550                 555

cga atc atg gaa tcc ctt gca tgg ctc tca gat tca cct tta ttt gat    1850
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
            560             565                 570

ctt att aaa caa tca aag gac cga gaa gga cca act gat cac ctt gaa    1898
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
            575             580                 585

tct gct tgt cct ctt aat ctt cct ctc cag aat aat cac act gca gca    1946
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
            590             595                 600

gat atg tat ctt tct cct gta aga tct cca aag aaa aaa ggt tca act    1994
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
            605             610                 615

acg cgt gta aat tct act gca aat gca gag aca caa gca acc tca gcc    2042
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
620             625                 630                 635

ttc cag acc cag aag cca ttg aaa tct acc tct ctt tca ctg ttt tat    2090
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
            640             645                 650

aaa aaa gtg tat cgg cta gcc tat ctc cgg cta aat aca ctt tgt gaa    2138
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
            655             660                 665

cgc ctt ctg tct gag cac cca gaa tta gaa cat atc atc tgg acc ctt    2186
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
            670             675                 680

ttc cag cac acc ctg cag aat gag tat gaa ctc atg aga gac agg cat    2234
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
            685             690                 695

ttg gac caa att atg atg tgt tcc atg tat ggc ata tgc aaa gtg aag    2282
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
700             705                 710                 715
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aat ata gac ctt aaa ttc aaa atc att gta aca gca tac aag gat ctt      2330
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
            720             725             730

cct cat gct gtt cag gag aca ttc aaa cgt gtt ttg atc aaa gaa gag      2378
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
            735             740             745

gag tat gat tct att ata gta ttc tat aac tcg gtc ttc atg cag aga      2426
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
            750             755             760

ctg aaa aca aat att ttg cag tat gct tcc acc agg ccc cct acc ttg      2474
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
            765             770             775

tca cca ata cct cac att cct cga agc cct tac aag ttt cct agt tca      2522
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780             785             790             795

ccc tta cgg att cct gga ggg aac atc tat att tca ccc ctg aag agt      2570
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
            800             805             810

cca tat aaa att tca gaa ggt ctg cca aca cca aca aaa atg act cca      2618
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
            815             820             825

aga tca aga atc tta gta tca att ggt gaa tca ttc ggg act tct gag      2666
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
            830             835             840

aag ttc cag aaa ata aat cag atg gta tgt aac agc gac cgt gtg ctc      2714
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
            845             850             855

aaa aga agt gct gaa gga agc aac cct cct aaa cca ctg aaa aaa cta      2762
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860             865             870             875

cgc ttt gat att gaa gga tca gat gaa gca gat gga agt aaa cat ctc      2810
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
            880             885             890

cca gga gag tcc aaa ttt cag cag aaa ctg gca gaa atg act tct act      2858
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
            895             900             905

cga aca cga atg caa aag cag aaa atg aat gat agc atg gat acc tca      2906
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
            910             915             920

aac aag gaa gag aaa tga ggatctcagg accttggtgg acactgtgta           2954
Asn Lys Glu Glu Lys  *
925


cacctctgga ttcattgtct ctcacagatg tgactgtata actttcccag gttctgttta   3014
tggccacatt taatatcttc agctcttttt gtggatataa aatgtgcaga tgcaattgtt   3074
tgggtgattc ctaagccact tgaaatgtta gtcattgtta tttatacaag attgaaaatc   3134
ttgtgtaaat cctgccattt aaaaagttgt agcagattgt ttcctcttcc aaagtaaaat   3194
tgctgtgctt tatggatagt aagaatggcc ctagagtggg agtcctgata acccaggcct   3254
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ttccaaatgc aatttgattg actgcccatt caccaaaatt atcctgaact cttctgcaaa   3434
aatggatatt attagaaatt agaaaaaaat tactaatttt acacattaga ttttattttta   3494
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cagaatgtaa aagaacttac tgattatttt cttcatccaa cttatgtttt taaatgagga   3674
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ggaatggtac atgtcttcca tgtatctttt gaactggcaa ttgtctattt atcttttatt   4034
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aaaagcttca aattaaaaca gctgcattag aaaaagaggc gcttctcccc tcccctacac   4214
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ataggggata tttaaggtag cttcagctag cttttaggaa aatcactttg tctaactcag   4334
aattattttt aaaaagaaat ctggtcttgt tagaaaacaa aattttattt tgtgctcatt   4394
taagtttcaa acttactatt ttgacagtta ttttgataac aatgacacta gaaaacttga   4454
ctccatttca tcattgtttc tgcatgaata tcatacaaat cagttagttt ttaggtcaag   4514
ggcttactat ttctgggtct tttgctacta agttcacatt agaattagtg ccagaatttt   4574
aggaacttca gagatcgtgt attgagattt cttaaataat gcttcagata ttattgcttt   4634
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aattaatagt ttgtctattt taaaataaat tagttgttaa gagtcttaat ggtctgatgt   4754
tgtgttcttt gtattaagta cactaatgtt ctcttttctg tctaggagaa gatagataga   4814
agataactct cctagtatct catcc                                          4839
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<210> 8
<211> 928
<212> PRT
<213> Homo sapien

<400> 8

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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1               5                   10                  15
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp
            20                  25                  30
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
            35                  40                  45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
    50                  55                  60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65                  70                  75                  80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
                85                  90                  95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
            100                 105                 110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
            115                 120                 125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
            130                 135                 140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145                 150                 155                 160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
            165                 170                 175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
            180                 185                 190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
            195                 200                 205
```

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Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
    210                 215                 220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225                 230                 235                 240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
                245                 250                 255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
            260                 265                 270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
        275                 280                 285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
    290                 295                 300
Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305                 310                 315                 320
Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
                325                 330                 335
Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
            340                 345                 350
Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
            355                 360                 365
Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
    370                 375                 380
Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385                 390                 395                 400
Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
            405                 410                 415
Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
            420                 425                 430
Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
        435                 440                 445
Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
    450                 455                 460
Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465                 470                 475                 480
Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
            485                 490                 495
Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
            500                 505                 510
Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
        515                 520                 525
Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
    530                 535                 540
Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545                 550                 555                 560
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
            565                 570                 575
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
            580                 585                 590
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
            595                 600                 605
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
    610                 615                 620
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625                 630                 635                 640
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
            645                 650                 655
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
            660                 665                 670
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
    675                 680                 685
```

```
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690             695         700
Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705             710         715                 720
Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
            725         730                 735
Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
            740         745         750
Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
        755         760             765
Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770             775         780
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785             790             795                 800
Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
            805             810             815
Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820             825             830
Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
        835             840             845
Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850             855             860
Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865             870             875                 880
Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
            885             890             895
Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
            900             905             910
Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
    915             920             925
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<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
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      Oligonucleotide

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ttctgtagtt taattttctg aacctttggc   30

<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: note =
      synthetic construct

<400> 10
tcagccgaag agcttcagga agcaggg   27

<210> 11
<211> 32
<212> PRT
<213> Homo sapien

<220>

<221> VARIANT
<222> 2-3, 5-13, 15, 17-18, 20-21, 23-28, 30-31
<223> Xaa can be any amino acid

<400> 11
Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa His
 1   5   10   15
Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
          20   25   30

<210> 12
<211> 50
<212> PRT
<213> Homo sapien

<220>
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<222> 2-3, 5-20, 22-23, 25-26, 28-29, 31-46, 48-49
<223> Xaa can be any amino acid

<400> 12
Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10   15
Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa
          20   25   30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
          35   40   45
Xaa Cys
    50

<210> 13
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

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ggggagcggg gagggaatac ctaagagcaa ttggtagctg gtacttctaa tgcctcttcc   120
tcctccaacc tccaagagtc tgttttggga ttgggttcag gaatgaaatt ctgcctgtgc   180
taacctcctg gggagccggt agacttgtct gttaaaaatc gcttctgctt ttggagccta   240
aagcccggtt ccgaaaaaca agtggtattt aggggaaaga ggggtcttca aaggctacag   300
tgagtcattc cagccttcaa ccatactacg ccagcactac gttctctaaa gccactctgc   360
gctagcttgc ggtgagggga ggggagaaaa ggaaagggga ggggagggga ggggagggag   420
aaaggaggtg ggaaggcaga gaggccggct gcggggggcgg gaccgactca caaactgttc   480
gatttcgttt ccacctccca gcgccccctc ggagatccct aggagccagc ctgctgggag   540
aaccagaggg tccggagcaa acctggaggc tgagagggca tcagagggga aaagactgag   600
ctagccactc cagtgccata cagaagctta agggacgcac cacgccagcc ccagcccagc   660
gacagccaac gcctgttgca gagcggcggc ttcgaagccg ccgcccagga gctgcccttt   720
cctcttcggt gaagtttcta aaagctgcgg gagactcaga ggaagcaagg aaagtgtccg   780
gtaggactac ggctgccttt gtcctcttcc cctctaccct taccccctcc tgggtcccct   840
ctccaggagc tgactaggca ggctttctgg ccaaccctct cccctacacc cccagctctg   900
ccagccagtt tgcacagagg taaactccct ttggctgaga gtaggggagc ttgttgcaca   960
ttgcaaggaa ggcttttggg agcccagaga ctgaggagca acagcacgcc caggagagtc   1020
cctggttcca ggttctcgcc cctgcacctc ctcctgcccg cccctcaccc tgtgtgtggt   1080
gttagaaatg aaaagatgaa aaggcagcta gggtttcagt agtcgaaagc aaaacaaaag   1140
ctaaaagaaa acaaaaagaa aatagcccag ttcttatttg cacctgcttc agtggacttt   1200
gaatttggaa ggcagaggat ttccccttttt ccctcccgtc aaggtttgag catcttttaa   1260

```
tctgttcttc aagtatttag agacaaactg tgtaagtagc agggcagatc ctgtcttgcg    1320
cgtgccttcc tttactggag actttgaggt tatctgggca ctcccccac ccacccccc    1380
tcctgcaagt tttcttcccc ggagcttccc gcaggtgggc agctagctgc agatactaca    1440
tcatcagtca ggagaactct tcagagcaag agacgaggag gcaggataag ggaattc       1497
```

<210> 14
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
       synthetic construct

<400> 14
```
ctgcagcttg ttctttaatg tcaggagact ctcccttctg cttgtcctgg tgggccctgg     60
ggggagcggg gagggaatac ctaagagcaa ttggtagctg gtacttctaa tgcctcttcc    120
tcctccaacc tccaagagtc tgttttggga ttgggttcag gaatgaaatt ctgcctgtgc    180
taacctcctg gggagccggt agacttgtct gttaaaaatc gcttctgctt ttggagccta    240
aagcccggtt ccgaaaaaca agtggtattt aggggaaaga ggggtcttca aaggctacag    300
tgagtcattc cagccttcaa ccatactacg ccagcactac gttctctaaa gccactctgc    360
gctagcttgc ggtgagggga ggggagaaaa ggaaagggga ggggagggga ggggaggggag    420
aaaggaggtg ggaaggcaga gaggccggct gcggggggcgg gaccgactca caaactgttc    480
gatttcgttt ccacctccca gcgcccctc ggagatccct aggagccagc ctgctgggag    540
aaccagaggg tccggagcaa acctggaggc tgagagggca tcagagggga aaagactgag    600
```

<210> 15
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
       synthetic construct

<400> 15
```
cccaagcgct agtgttctgt tctcttttg taatcttgga atcttttgtt gctctaaata     60
caattaaaaa tggcagaaac ttgtttgttg gaatacatgt gtgactcttg gtttgtctct    120
gcgtctggct ttagaaatgt catccattgt gtaaaatact ggcttgttgg tctgccagct    180
aaaacttgcc acagccctg ttgtgactgc aggctcaagt tattgttaac aaagagcccc    240
aagaaaagct gctaatgtcc tcttatcacc attgttaatt tgttaaaaca taaaacaatc    300
taaaatttca gatgaatgtc atcagagttc ttttcattag ctcttttat ggctgtct      359
```

<210> 16
<211> 899
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
       synthetic construct

<400> 16
```
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1               5                   10                  15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25                  30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
        35                  40                  45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
    50                  55                  60
```

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```
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65              70              75              80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
            85              90              95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
        100             105             110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
        115             120             125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
    130             135             140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145             150             155             160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
            165             170             175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
        180             185             190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
    195             200             205
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
    210             215             220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225             230             235             240
Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu
            245             250             255
Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val
        260             265             270
Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu
        275             280             285
Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser
    290             295             300
Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys
305             310             315             320
Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser
            325             330             335
Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr
        340             345             350

Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro
    355             360             365
His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn
    370             375             380
Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Gln Cys Arg
385             390             395             400
Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser
            405             410             415
Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe
            420             425             430
Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Gly Ser
        435             440             445
Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg
    450             455             460
Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu
465             470             475             480
Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro
            485             490             495
Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly
        500             505             510
Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
        515             520             525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530             535             540
```

```
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545             550             555             560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
            565             570             575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
        580             585             590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
        595             600             605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610             615             620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625             630             635             640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
            645             650             655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
            660             665             670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
        675             680             685       .
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
        690             695             700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705             710             715             720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
            725             730             735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
            740             745             750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
            755             760             765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
            770             775             780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785             790             795             800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
            805             810             815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
            820             825             830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
            835             840             845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850             855             860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865             870             875             880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
            885             890             895
His Thr Gln
```

<210> 17
<211> 2988
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 17

```
gcttcccgca ggtgggcagc tagctgcaga tactacatca tcagtcagga gaactcttca    60
gagcaagaga cgaggaggca ggataaggga attcggtgga agctacagac aagctcaagg   120
atggaggtgc agttagggct gggaagggtc tacccacggc ccccatccaa gacctatcga   180
ggagcgttcc agaatctgtt ccagagcgtg cgcgaagcga tccagaaccc gggccccagg   240
```

```
caccctgagg ccgctaacat agcacctccc ggcgcctgtt tacagcagag gcaggagact      300
agcccccggc ggcggcggcg gcagcagcac actgaggatg gttctcctca agcccacatc      360
agaggcccca caggctacct ggccctggag gaggaacagc agccttcaca gcagcaggca      420
gcctccgagg gccaccctga gagcagctgc ctccccgagc ctggggcggc caccgctcct      480
ggcaaggggc tgccgcagca gccaccagct cctccagatc aggatgactc agctgcccca      540
tccacgttgt ccctgctggg ccccactttc ccaggcttaa gcagctgctc cgccgacatt      600
aaagacattt tgaacgaggc cggcaccatg caacttcttc agcagcagca acaacagcag      660
cagcaccaac agcagcacca acagcaccaa cagcagcagg aggtaatctc cgaaggcagc      720
agcgcaagag ccagggaggc cacggggggct ccctcttcct ccaaggatag ttacctaggg      780
ggcaattcaa ccatatctga cagtgccaag gagttgtgta aagcagtgtc tgtgtccatg      840
ggattgggtg tggaagcatt ggaacatctg agtccagggg aacagcttcg gggagactgc      900
atgtacgcgt cgctcctggg aggtccaccc gcggtgcgtc ccactccttg tgcgccgctg      960
cccgaatgca aaggtcttcc cctggacgaa ggcccaggca aaagcactga agagactgct     1020
gagtattcct ctttcaaggg aggttacgcc aaaggattgg aaggtgagag cttgggggtgc     1080
tctggcagca gtgaagcagg tagctctggg acacttgaga tcccgtcctc tctgtctctg     1140
tataaatctg gagcactaga cgaggcagca gcataccaga atcgcgacta ctacaacttt     1200
ccgctggctc tgtccgggcc gccgcacccc ccgcccccta cccatccaca cgcccgtatc     1260
aagctggaga acccattgga ctacggcagc gcctgggctg cggcggcagc gcaatgccgc     1320
tatggggact tgggtagtct acatggaggg agtgtagccg gcccagcac tggatcgccc     1380
ccagccacca cctcttcttc ctggcatact ctcttcacag ctgaagaagg ccaattatat     1440
gggccaggag gcggggggcgg cagcagcagc ccaagcgatg ccgggcctgt agcccctat     1500
ggctacactc ggcccctca ggggctgaca gccaggaga gtgactactc tgcctccgaa     1560
gtgtggtatc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa     1620
agtgaaatgg gaccttggat ggagaactac tccggacctt atggggacat gcgtttggac     1680
agtaccaggg accatgtttt acccatcgac tattactttc caccccagaa gacctgcctg     1740
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag     1800
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat     1860
tgtaccattg ataaatttcg gaggaaaaat tgcccatctt gtcgtctccg gaaatgttat     1920
gaagcaggga tgactctggg agctcgtaag ctgaagaaac ttggaaatct aaaactacag     1980
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact     2040
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt     2100
gagccaggag tggtgtgtgc cggacatgac aacaaccaac agattccttt gctgccttg     2160
ttatctagcc tcaatgagct tggagagagg cagcttgtgc atgtggtcaa gtgggccaag     2220
gccttgcctg gcttccgcaa cttgcatgtg gatgaccaga tggcggtcat tcagtattcc     2280
tggatgggac tgatggtatt tgccatgggt tggcggtcct tcactaatgt caactccagg     2340
atgctctact ttgcacctga cttggttttc aatgagtacc gcatgcacaa gtctcggatg     2400
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc     2460
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg     2520
ctgaaaaatc aaaaattctt tgatgaactt cgaatgaact acatcaagga actcgatcgc     2580
atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc     2640
aagctcctgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg     2700
ctaatcaagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct     2760
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga     2820
agatttggaa accctaatac ccaaaaccca ccttgttccc tttccagatg tcttctgcct     2880
gttatataac tctgcactac ttctctgcag tgccttgggg gaaattcctc tactgatgta     2940
cagtcagacg tgaacaggtt cctcagttct atttcctggg cttctcct              2988
```

<210> 18
<211> 899
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 18
```
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1               5                   10                  15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25                  30
```

Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
        35   40   45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
    50   55   60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65   70   75   80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
            85   90   95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
        100   105   110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
        115   120   125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
    130   135   140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145   150   155   160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
            165   170   175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
        180   185   190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
    195   200   205
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
    210   215   220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225   230   235   240
Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu
            245   250   255
Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val
        260   265   270
Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu
    275   280   285
Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser
    290   295   300
Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys
305   310   315   320
Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser
            325   330   335
Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr
        340   345   350
Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro
    355   360   365
His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn
    370   375   380
Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Gln Cys Arg
385   390   395   400
Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser
            405   410   415
Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe
        420   425   430
Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Gly Ser
        435   440   445
Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg
    450   455   460
Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu
465   470   475   480
Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro
            485   490   495
Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly
            500   505   510

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```
Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
        515                 520                 525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530                 535                 540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545                     550                 555                 560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
                565                 570                 575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
                580                 585                 590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
            595                 600                 605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610                 615                 620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625                 630                 635                 640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
            645                 650                 655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
            660                 665                 670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
            675                 680                 685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
    690                 695                 700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705                 710                 715                 720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
            725                 730                 735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
            740                 745                 750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
        755                 760                 765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
    770                 775                 780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785                 790                 795                 800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
                805                 810                 815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
            820                 825                 830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
        835                 840                 845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850                 855                 860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865                 870                 875                 880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
                885                 890                 895
His Thr Gln
```

<210> 19
<211> 2988
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 19

```
gcttccccgca ggtgggcagc tagctgcaga tactacatca tcagtcagga gaactcttca    60
gagcaagaga cgaggaggca ggataaggga attcggtgga agctacagac aagctcaagg   120
atggaggtgc agttagggct gggaagggtc tacccacggc ccccatccaa gacctatcga   180
ggagcgttcc agaatctgtt ccagagcgtg cgcgaagcga tccagaaccc gggcccccagg   240
caccctgagg ccgctaacat agcacctccc ggcgcctgtt tacagcagag gcaggagact   300
agcccccggc ggcggcggcg gcagcagcac actgaggatg gttctcctca gcccacatc    360
agaggcccca caggctacct ggccctggag gaggaacagc agccttcaca gcagcaggca   420
gcctccgagg gccaccctga gagcagctgc ctccccgagc ctggggcggc caccgctcct   480
ggcaagggc tgccgcagca gccaccagct cctccagatc aggatgactc agctgcccca   540
tccacgttgt ccctgctggg ccccactttc ccaggcttaa gcagctgctc cgccgacatt   600
aaagacattt tgaacgaggc cggcaccatg caacttcttc agcagcagca acaacagcag   660
cagcaccaac agcagcacca acagcaccaa cagcagcagg aggtaatctc cgaaggcagc   720
agcgcaagag ccagggaggc cacggggggct ccctcttcct ccaaggatag ttacctaggg   780
ggcaattcaa ccatatctga cagtgccaag gagttgtgta aagcagtgtc tgtgtccatg   840
ggattgggtg tggaagcatt ggaacatctg agtccagggg aacagcttcg gggagactgc   900
atgtacgcgt cgctcctggg aggtccaccc gcggtgcgtc ccactccttg tgcgccgctg   960
cccgaatgca aaggtcttcc cctggacgaa ggcccaggca aaagcactga agagactgct  1020
gagtattcct cttttcaaggg aggttacgcc aaaggattgg aaggtgagag cttggggtgc  1080
tctggcagca gtgaagcagg tagctctggg acacttgaga tcccgtcctc tctgtctctg  1140
tataaatctg agcactaga cgaggcagca gcataccaga atcgcgacta ctacaacttt  1200
ccgctggctc tgtccgggcc gccgcacccc ccgcccccta cccatccaca cgcccgtatc  1260
aagctggaga acccattgga ctacggcagc gcctgggctg cggcggcagc gcaatgccgc  1320
tatggggact tgggtagtct acatggaggg agtgtagccg ggcccagcac tggatcgccc  1380
ccagccacca cctcttcttc ctggcatact ctcttcacag ctgaagaagg ccaattatat  1440
gggccaggag gcggggggcgg cagcagcagc ccaagcgatg ccgggcctgt agcccccctat  1500
ggctacactc ggccccctca ggggctgaca agccaggaga gtgactactc tgcctccgaa  1560
gtgtggtatc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa  1620
agtgaaatgg gaccttggat ggagaactac tccggacctt atggggacat gcgtttggac  1680
agtaccaggg accatgtttt acccatcgac tattacttc caccccagaa gacctgcctg  1740
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag  1800
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat  1860
tgtaccattg ataaatttcg gaggaaaaat tgcccatctt gtcgtctccg gaaatgttat  1920
gaagcaggga tgactctggg agctcgtaag ctgaagaaac ttggaaatct aaaactacag  1980
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact  2040
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt  2100
gagccaggag tggtgtgtgc cggacatgac aacaaccaac agattccttt gctgccttg  2160
ttatctagcc tcaatgagct tggagagagg cagcttgtgc atgtggtcaa gtgggccaag  2220
gccttgcctg cttccgcaa cttgcatgtg gatgaccaga tggcggtcat tcagtattcc  2280
tggatgggac tgatggtatt tgccatgggt tggcggtcct tcactaatgt caactccagg  2340
atgctctact ttgcacctga cttggttttc aatgagtacc gcatgcacaa gtctcggatg  2400
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc  2460
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg  2520
ctgaaaaatc aaaaattctt tgatgaactt cgaatgaact acatcaagga actcgatcgc  2580
atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc  2640
aagctcctgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg  2700
ctaatcaagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct  2760
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga  2820
agatttggaa accctaatac ccaaaaccca ccttgttccc tttccagatg tcttctgcct  2880
gttatataac tctgcactac ttctctgcag tgccttgggg gaaattcctc tactgatgta  2940
cagtcagacg tgaacaggtt cctcagttct atttcctggg cttctcct              2988
```

<210> 20
<211> 899
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 20

```
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1               5                   10          15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25              30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
        35              40              45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
    50              55              60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65              70                  75              80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
            85                  90                  95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
        100             105             110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
    115             120             125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
    130             135             140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145             150             155             160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
            165             170             175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
        180             185             190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
    195             200             205
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
    210             215             220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225             230             235             240
Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu
            245             250             255
Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val
            260             265             270
Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu
            275             280             285
Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser
    290             295             300
Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys
305             310             315             320
Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser
            325             330             335
Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr
            340             345             350
Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro
        355             360             365
His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn
    370             375             380
Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg
385             390             395             400
Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser
            405             410             415
Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe
            420             425             430
Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Gly Ser
        435             440             445
Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg
    450             455             460
Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu
465             470             475             480
```

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```
Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro
             485             490             495
Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly
             500             505             510
Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
             515             520             525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530             535             540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545             550             555             560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
             565             570             575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
             580             585             590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
             595             600             605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610             615             620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625             630             635             640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
             645             650             655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
             660             665             670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
             675             680             685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
             690             695             700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705             710             715             720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
             725             730             735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
             740             745             750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
             755             760             765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
    770             775             780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785             790             795             800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
             805             810             815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
             820             825             830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
             835             840             845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850             855             860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865             870             875             880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
             885             890             895
His Thr Gln
```

<210> 21
<211> 2700
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 21
```
atggaggtgc agttagggct gggaagggtc tacccacggc ccccatccaa gacctatcga      60
ggagcgttcc agaatctgtt ccagagcgtg cgcgaagcga tccagaaccc gggccccagg     120
caccctgagg ccgctaacat agcacctccc ggcgcctgtt tacagcagag gcaggagact     180
agcccccggc ggcggcggcg gcagcagcac actgaggatg gttctcctca agcccacatc     240
agaggcccca caggctacct ggccctggag gaggaacagc agccttcaca gcagcaggca     300
gcctccgagg gccaccctga gagcagctgc ctccccgagc ctggggcggc caccgctcct     360
ggcaagggggc tgccgcagca gccaccagct cctccagatc aggatgactc agctgcccca     420
tccacgttgt ccctgctggg ccccactttc ccaggcttaa gcagctgctc cgccgacatt     480
aaagacattt tgaacgaggc cggcaccatg caacttcttc agcagcagca acaacagcag     540
cagcaccaac agcagcacca acagcaccaa cagcagcagg aggtaatctc cgaaggcagc     600
agcgcaagag ccagggaggc cacgggggct ccctcttcct ccaaggatag ttacctaggg     660
ggcaattcaa ccatatctga cagtgccaag gagttgtgta aagcagtgtc tgtgtccatg     720
ggattgggtg tggaagcatt ggaacatctg agtccagggg aacagcttcg gggagactgc     780
atgtacgcgt cgctcctggg aggtccaccc gcggtgcgtc ccactccttg tgcgccgctg     840
cccgaatgca aaggtcttcc cctggacgaa ggcccaggca aagcactga agagactgct     900
gagtattcct ctttcaaggg aggttacgcc aaaggattgg aaggtgagag cttggggtgc     960
tctggcagca gtgaagcagg tagctctggg acacttgaga tcccgtcctc tctgtctctg    1020
tataaatctg agcactaga cgaggcagca gcataccaga atcgcgacta ctacaacttt    1080
ccgctggctc tgtccgggcc gccgcacccc ccgcccccta cccatccaca cgcccgtatc    1140
aagctggaga acccattgga ctacggcagc gcctgggctg cggcggcagc gcaatgccgc    1200
tatggggact tgggtagtct acatggaggg agtgtagccg ggcccagcac tggatcgccc    1260
ccagccacca cctcttcttc ctggcatact ctcttcacag ctgaagaagg ccaattatat    1320
gggccaggag gcggggggcgg cagcagcagc ccaagcgatg ccgggcctgt agcccccctat    1380
ggctacactc ggccccctca ggggctgaca agccaggaga gtgactactc tgcctccgaa    1440
gtgtggtacc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa    1500
agtgaaatgg accttggat ggagaactac tccggacctt atggggacat gcgtttggac    1560
agtaccaggg accatgtttt acccatcgac tattactttc caccccagaa gacctgcctg    1620
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag    1680
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat    1740
tgtaccattg ataaatttcg gaggaaaaat tgcccatctt gtcgtctccg gaaatgttat    1800
gaagcaggga tgactctggg agctcgtaag ctgaagaaac ttggaaatct aaaactacag    1860
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact    1920
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt    1980
gagccaggag tggtgtgtgc cggacatgac aacaaccaac agattccttt gctgccttg    2040
ttatctagcc tcaatgagct tggagagagg cagcttgtgc atgtggtcaa gtgggccaag    2100
gccttgcctg gcttccgcaa cttgcatgtg gatgaccaga tggcggtcat tcagtattcc    2160
tggatgggac tgatggtatt tgccatgggt tggcggtcct tcactaatgt caactccagg    2220
atgctctact ttgcacctga cttggttttc aatgagtacc gcatgcacaa gtctcggatg    2280
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc    2340
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg    2400
ctgaaaaatc aaaaattctt tgatgaactt cgaatgaact acatcaagga actcgatcgc    2460
atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc    2520
aagctcctgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg    2580
ctaatcaagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct    2640
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga    2700
```

<210> 22
<211> 4321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 22
```
cgagatcccg gggagccagc ttgctgggag agcgggacgg tccggagcaa gcccacaggc      60
```

```
agaggaggcg acagagggaa aaagggccga gctagccgct ccagtgctgt acaggagccg    120
aagggacgca ccacgccagc cccagcccgg ctccagcgac agccaacgcc tcttgcagcg    180
cggcggcttc gaagccgccg cccggagctg ccctttcctc ttcggtgaag tttttaaaag    240
ctgctaaaga ctcggaggaa gcaaggaaag tgcctggtag gactgacggc tgcctttgtc    300
ctcctcctct ccacccgcc tcccccacc ctgccttccc ccctcccc gtcttctctc        360
ccgcagctgc ctcagtcggc tactctcagc caacccccct caccacccctt ctccccaccc  420
gccccccgc ccccgtcggc ccagcgctgc cagcccgagt ttgcagagag gtaactccct     480
ttggctgcga gcgggcgagc tagctgcaca ttgcaaagaa ggctcttagg agccaggcga    540
ctggggagcg gcttcagcac tgcagccacg acccgcctgg ttagaattcc ggcggagaga    600
accctctgtt ttcccccact ctctctccac ctcctcctgc cttccccacc ccgagtgcgg    660
agcagagatc aaaagatgaa aaggcagtca ggtcttcagt agccaaaaaa caaaacaaac    720
aaaaacaaaa aagccgaaat aaaagaaaaa gataataact cagttcttat ttgcacctac    780
ttcagtggac actgaatttg gaaggtggag gattttgttt ttttctttta agatctgggc    840
atcttttgaa tctacccttc aagtattaag agacagactg tgagcctagc agggcagatc    900
ttgtccaccg tgtgtcttct tctgcacgag actttgaggc tgtcagagcg cttttttgcgt  960
ggttgctccc gcaagtttcc ttctctggag cttcccgcag gtgggcagct agctgcagcg   1020
actaccgcat catcacagcc tgttgaactc ttctgagcaa gagaagggga ggcggggtaa   1080
gggaagtagg tggaagattc agccaagctc aaggatggaa gtgcagttag ggctgggaag   1140
ggtctaccct cggccgccgt ccaagaccta ccgaggagct ttccagaatc tgttccagag   1200
cgtgcgcgaa gtgatccaga acccgggccc caggcaccca gaggccgcga gcgcagcacc   1260
tcccggcgcc agtttgctgc tgctgcagca gcagcagcag cagcagcagc agcagcagca   1320
gcagcagcag cagcagcagc agcagcaaga gactagcccc aggcagcagc agcagcagca   1380
gggtgaggat ggttctcccc aagcccatcg tagaggcccc acaggctacc tggtcctgga   1440
tgaggaacag caaccttcac agccgcagtc ggccctggag tgccaccccg agagaggttg   1500
cgtcccagag cctggagccg ccgtggccgc cagcaagggg ctgccgcagc agctgccagc   1560
acctccggac gaggatgact cagctgcccc atccacgttg tccctgctgg gccccacttt   1620
ccccggctta agcagctgct ccgctgacct taaagacatc ctgagcgagg ccagcaccat   1680
gcaactcctt cagcaacagc agcaggaagc agtatccgaa ggcagcagca gcgggagagc   1740
gagggaggcc tcggggggctc ccacttcctc caaggacaat tacttagggg gcacttcgac   1800
catttctgac aacgccaagg agttgtgtaa ggcagtgtcg gtgtccatgg cctgggtgt    1860
ggaggcgttg gagcatctga gtccagggga acagcttcgg ggggattgca tgtacgcccc   1920
actttgggga gttccacccg ctgtgcgtcc cactccttgt gccccattgg ccgaatgcaa   1980
aggttctctg ctagacgaca gcgcaggcaa gagcactgaa gatactgctg agtattcccc   2040
tttcaaggga ggttacacca aagggctaga aggcgagagc ctaggctgct ctggcagcgc   2100
tgcagcaggg agctccggga cacttgaact gccgtctacc ctgtctctct acaagtccgg   2160
agcactggac gaggcagctg cgtaccagag tcgcgactac tacaactttc cactggctct   2220
ggccggaccg ccgcccctc cgccgcctcc ccatccccac gctcgcatca agctggagaa    2280
cccgctggac tacggcagcg cctgggcggc tgcggcggcg cagtgccgct atggggacct   2340
ggcgagcctg catggcgcgg gtgcagcggg acccggttct gggtcaccct cagccgccgc   2400
ttcctcatcc tggcacactc tcttcacagc cgaagaaggc cagttgtatg accgtgtgg    2460
tggtggtggg ggtggtggcg gcggcggcgg cggcggcggc ggcggcggcg gcggcggcgg   2520
cggcggcggc gaggcgggag ctgtagcccc ctacggctac actcggcccc ctcaggggct   2580
ggcgggccag gaaagcgact tcaccgcacc tgatgtgtgg taccctggcg gcatggtgag   2640
cagagtgccc tatcccagtc ccacttgtgt caaaagcgaa atgggcccct ggatggatag   2700
ctactccgga ccttacgggg acatgcgttt ggagactgcc agggaccatg ttttgcccat   2760
tgactattac tttccacccc agaagacctg cctgatctgt ggagatgaag cttctgggtg   2820
tcactatgga gctctcacat gtggaagctg caaggtcttc ttcaaaagag ccgctgaagg   2880
gaaacagaag tacctgtgcg ccagcagaaa tgattgcact attgataaat tccgaaggaa   2940
aaattgtcca tcttgtcgtc ttcggaaatg ttatgaagca gggatgactc tgggagcccg   3000
gaagctgaag aaacttggta atctgaaact acaggaggaa ggagaggctt ccagcaccac   3060
cagccccact gaggagacaa cccagaagct gacagtgtca cacattgaag ctatgaatg    3120
tcagcccatc tttctgaatg tcctggaagc cattgagcca ggtgtagtgt gtgctggaca   3180
cgacaacaac cagcccgact cctttgcagc cttgctctct agcctcaatg aactgggaga   3240
gagacagctt gtacacgtgg tcaagtgggc caaggccttg cctggcttcc gcaacttaca   3300
cgtggacgac cagatggctg tcattcagta ctcctggatg gggctcatgg tgtttgccat   3360
gggctggcga tccttcacca atgtcaactc caggatgctc tacttcgccc ctgatctggt   3420
tttcaatgag taccgcatgc acaagtcccg gatgtacagc cagtgtgtcc gaatgaggca   3480
cctctctcaa gagtttggat ggctccaaat cacccccag gaattcctgt gcatgaaagc    3540
actgctactc ttcagcatta ttccagtgga tgggctgaaa aatcaaaaat tctttgatga   3600
acttcgaatg aactacatca aggaactcga tcgtatcatt gcatgcaaaa gaaaaaatcc   3660
cacatcctgc tcaagacgct tctaccagct caccaagctc ctggactccg tgcagcctat   3720
```

29

```
tgcgagagag ctgcatcagt tcacttttga cctgctaatc aagtcacaca tggtgagcgt   3780
ggactttccg gaaatgatgg cagagatcat ctctgtgcaa gtgcccaaga tcctttctgg   3840
gaaagtcaag cccatctatt ccacacccca gtgaagcatt ggaaaccota tttccccacc   3900
ccagctcatg cccccttttca gatgtcttct gcctgttata actctgcact actcctctgc   3960
agtgccttgg ggaatttcct ctattgatgt acagtctgtc atgaacatgt tcctgaattc   4020
tatttgctgg gctttttttt tctctttctc tcctttcttt ttcttcttcc ctccctatct   4080
aaccctccca tggcaccttc agactttgct tcccattgtg gctcctatct gtgttttgaa   4140
tggtgttgta tgcctttaaa tctgtgatga tcctcatatg cccagtgtc aagttgtgct   4200
tgtttacagc actactctgt gccagccaca caaacgttta cttatcttat gccacgggaa   4260
gtttagagag ctaagattat ctggggaaat caaaacaaaa aacaagcaaa caaaaaaaaa   4320
a                                                                   4321
```

<210> 23
<211> 919
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 23
```
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1               5                  10                  15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25                  30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
        35                  40                  45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
    50                  55                  60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
65                  70                  75                  80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
                85                  90                  95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
            100                 105                 110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
            115                 120                 125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
    130                 135                 140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
145                 150                 155                 160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
                165                 170                 175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
            180                 185                 190
Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
            195                 200                 205
Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
    210                 215                 220
Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
225                 230                 235                 240
Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
                245                 250                 255
Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
            260                 265                 270
Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
    275                 280                 285
Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
    290                 295                 300
```

```
Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly
305                 310             315                 320
Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr
                325             330             335
Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
            340             345             350
Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
        355             360             365
Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
    370             375             380
Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
385             390             395                 400
Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
            405             410             415
Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser
            420             425             430
Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
        435             440             445
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
        450             455             460
Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr
465             470             475                 480
Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe
            485             490             495
Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro
            500             505             510
Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp
        515             520             525
Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp
    530             535             540
His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu
545             550             555                 560
Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
            565             570             575
Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys
        580             585             590
Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg
        595             600             605
Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met
    610             615             620
Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln
625             630             635                 640
Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr
            645             650             655
Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile
            660             665             670
Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
        675             680             685
His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
    690             695             700
Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
705             710             715                 720
Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
            725             730             735
Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
            740             745             750
Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
        755             760             765
Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
    770             775             780
```

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```
Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
785             790             795             800
Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
            805             810             815
Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
            820             825             830
Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
        835             840             845
Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
        850             855             860
Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
865             870             875             880
Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
            885             890             895
Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
            900             905             910
Pro Ile Tyr Phe His Thr Gln
            915


<210> 24
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 24
Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
 1               5                   10                  15
Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
            20                  25                  30
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
        35                  40                  45
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
    50                  55                  60
Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
65                  70                  75                  80
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
            85                  90                  95
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
            100             105             110
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
            115             120             125
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
        130             135             140
Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
145             150             155             160
Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
            165             170             175
Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
            180             185             190
Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
            195             200             205
Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
        210             215             220
Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
225             230             235             240
Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
            245             250             255
```

```
Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
        260             265                 270
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
        275             280                 285
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
    290             295                 300
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
305             310                 315                 320
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
            325             330                 335
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
        340             345                 350
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
        355             360                 365
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
    370             375                 380
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
385             390                 395                 400
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
            405             410                 415
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
        420             425                 430
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
        435             440                 445
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
    450             455                 460
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
465             470                 475                 480
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
            485             490                 495
Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
        500             505                 510
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
        515             520                 525
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
    530             535                 540
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545             550                 555                 560
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
            565             570                 575
His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
            580             585                 590
Ala Thr Val
        595
```

```
<210> 25
<211> 6450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 25
gagttgtgcc tggagtgatg tttaagccaa tgtcagggca aggcaacagt ccctggccgt      60
cctccagcac ctttgtaatg catatgagct cgggagacca gtacttaaag ttggaggccc     120
gggagcccag gagctggcgg agggcgttcg tcctgggagc tgcacttgct ccgtcgggtc     180
gccggcttca ccggaccgca ggctcccggg gcagggccgg ggccagagct cgcgtgtcgg     240
cgggacatgc gctgcgtcgc ctctaacctc gggctgtgct cttttttccag gtggcccgcc     300
ggtttctgag ccttctgccc tgcggggaca cggtctgcac cctgcccgcg gccacggacc     360
```

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atgaccatga ccctccacac caaagcatct gggatggccc tactgcatca gatccaaggg      420
aacgagctgg agcccctgaa ccgtccgcag ctcaagatcc ccctggagcg gcccctgggc      480
gaggtgtacc tggacagcag caagcccgcc gtgtacaact accccgaggg cgccgcctac      540
gagttcaacg ccgcggccgc cgccaacgcg caggtctacg gtcagaccgg cctcccctac      600
ggccccgggt ctgaggctgc ggcgttcggc tccaacggcc tggggggttt ccccccactc      660
aacagcgtgt ctccgagccc gctgatgcta ctgcacccgc cgccgcagct gtcgcctttc      720
ctgcagcccc acggccagca ggtgccctac tacctggaga acgagcccag cggctacacg      780
gtgcgcgagg ccggcccgcc ggcattctac aggccaaatt cagataatcg acgccagggt      840
ggcagagaaa gattggccag taccaatgac aagggaagta tggctatgga atctgccaag      900
gagactcgct actgtgcagt gtgcaatgac tatgcttcag gctaccatta tggagtctgg      960
tcctgtgagg gctgcaaggc cttcttcaag agaagtattc aaggacataa cgactatatg     1020
tgtccagcca ccaaccagtg caccattgat aaaaacagga ggaagagctg ccaggcctgc     1080
cggctccgca aatgctacga agtgggaatg atgaaaggtg ggatacgaaa agaccgaaga     1140
ggagggagaa tgttgaaaca caagcgccag agagatgatg gggaggggcag gggtgaagtg     1200
gggtctgctg gagacatgag agctgccaac ctttggccaa gcccgctcat gatcaaacgc     1260
tctaagaaga acagcctggc cttgtccctg acggccgacc agatggtcag tgccttgttg     1320
gatgctgagc cccccatact ctattccgag tatgatccta ccagacccct cagtgaagct     1380
tcgatgatgg gcttactgac caacctggca gacagggagc tggttcacat gatcaactgg     1440
gcgaagaggg tgccaggctt tgtggatttg accctccatg atcaggtcca ccttctagaa     1500
tgtgcctggc tagagatcct gatgattggt ctcgtctggc gctccatgga gcacccagtg     1560
aagctactgt ttgctcctaa cttgctcttg gacaggaacc agggaaaatg tgtagagggc     1620
atggtggaga tcttcgacat gctgctggct acatcatctc ggttccgcat gatgaatctg     1680
cagggagagg agtttgtgtg cctcaaatct attattttgc ttaattctgg agtgtacaca     1740
tttctgtcca gcaccctgaa gtctctggaa gagaaggacc atatccaccg agtcctggac     1800
aagatcacag acactttgat ccacctgatg gccaaggcag cctgaccct gcagcagcag     1860
caccagcggc tggcccagct cctcctcatc ctctcccaca tcaggcacat gagtaacaaa     1920
ggcatggagc atctgtacag catgaagtgc aagaacgtgg tgccctcta tgacctgctg     1980
ctggagatgc tggacgccca ccgcctacat gcgcccacta gccgtggagg ggcatccgtg     2040
gaggagacgg accaaagcca cttggccact gcgggctcta cttcatcgca ttccttgcaa     2100
aagtattaca tcacgggggga ggcagagggt ttccctgcca cagtctgaga gctccctggc     2160
tcccacacgg ttcagataat ccctgctgca ttttaccctc atcatgcacc actttagcca     2220
aattctgtct cctgcataca ctccggcatg catccaacac caatggcttt ctagatgagt     2280
ggccattcat ttgcttgctc agttcttagt ggcacatctt ctgtcttctg ttgggaacag     2340
ccaaagggat tccaaggcta aatctttgta acagctctct ttccccttg ctatgttact     2400
aagcgtgagg attcccgtag ctcttcacag ctgaactcag tctatgggtt ggggctcaga     2460
taactctgtg catttaagct acttgtagag acccaggcct ggagagtaga cattttgcct     2520
ctgataagca ctttttaaat ggctctaaga ataagccaca gcaaagaatt taaagtggct     2580
cctttaattg gtgacttgga gaaagctagg tcaagggttt attatagcac cctcttgtat     2640
tcctatggca atgcatcctt ttatgaaagt ggtacacctt aaagctttta tatgactgta     2700
gcagagtatc tggtgattgt caattcactt ccccctatag gaatacaagg ggccacacag     2760
ggaaggcaga tcccctagtt ggccaagact tattttaact tgatacactg cagattcaga     2820
gtgtcctgaa gctctgcctc tggctttccg gtcatgggtt ccagttaatt catgcctccc     2880
atggacctat ggagagcaac aagttgatct tagttaagtc tccctatatg agggataagt     2940
tcctgatttt tgttttatt tttgtgttac aaaagaaagc cctccctccc tgaacttgca     3000
gtaaggtcag cttcaggacc tgttccagtg ggcactgtac ttggatcttc ccggcgtgtg     3060
tgtgccttac acaggggtga actgttcact gtggtgatgc atgatgaggg taaatggtag     3120
ttgaaaggag caggggccct ggtgttgcat ttagccctgg ggcatggagc tgaacagtac     3180
ttgtgcagga ttgttgtggc tactagagaa caagagggaa agtagggcag aaactggata     3240
cagttctgag cacagccaga cttgctcagg tggccctgca caggctgcag ctacctagga     3300
acattccttg cagacccgc attgcctttg ggggtgccct gggatccctg gggtagtcca     3360
gctcttattc atttcccagc gtggccctgg ttggaagaag cagctgtcaa gttgtagaca     3420
gctgtgttcc tacaattggc ccagcaccct ggggcacggg agaagggtgg ggaccgttgc     3480
tgtcactact caggctgact ggggcctggt cagattacgt atgcccttgg tggtttagag     3540
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taaaaaagaa aggctcattc cagccacagg gcagccttcc ctgggccttt gcttctctag     3720
cacaattatg ggttacttcc tttttcttaa caaaaaagaa tgtttgattt cctctgggtg     3780
accttattgt ctgtaattga aaccctattg agaggtgatg tctgtgttag ccaatgaccc     3840
aggtagctgc tcgggcttct cttggtatgt cttgtttgga aaagtggatt tcattcattt     3900
ctgattgtcc agttaagtga tcaccaaagg actgagaatc tgggagggca aaaaaaaaaa     3960
aaaaagtttt tatgtgcact taaatttggg gacaattta tgtatctgtg ttaaggatat     4020
```

```
gcttaagaac ataattcttt tgttgctgtt tgtttaagaa gcaccttagt ttgtttaaga    4080
agcaccttat atagtataat atatatttt ttgaaattac attgcttgtt tatcagacaa      4140
ttgaatgtag taattctgtt ctggatttaa tttgactggg ttaacatgca aaaaccaagg     4200
aaaaatattt agtttttttt tttttttttg tatactttc aagctacctt gtcatgtata      4260
cagtcattta tgcctaaagc ctggtgatta ttcatttaaa tgaagatcac atttcatatc     4320
aactttgta tccacagtag acaaaatagc actaatccag atgcctattg ttggatattg      4380
aatgacagac aatcttatgt agcaaagatt atgcctgaaa aggaaaatta ttcagggcag     4440
ctaattttgc ttttaccaaa atatcagtag taatatttt ggacagtagc taatgggtca      4500
gtgggttctt tttaatgttt atacttagat tttcttttaa aaaaattaaa ataaaacaaa     4560
aaaaatttct aggactagac gatgtaatac cagctaaagc caaacaatta tacagtggaa     4620
ggttttacat tattcatcca atgtgtttct attcatgtta agatactact acatttgaag     4680
tgggcagaga acatcagatg attgaaatgt tcgcccaggg gtctccagca actttggaaa     4740
tctctttgta tttttacttg aagtgccact aatggacagc agatattttc tggctgatgt     4800
tggtattggg tgtaggaaca tgatttaaaa aaaaaactct tgcctctgct ttccccccact    4860
ctgaggcaag ttaaaatgta aaagatgtga tttatctggg gggctcaggt atggtgggga     4920
agtggattca ggaatctggg gaatggcaaa tatattaaga agagtattga aagtatttgg     4980
aggaaaatgg ttaattctgg gtgtgcacca aggttcagta gagtccactt ctgccctgga    5040
gaccacaaat caactagctc catttacagc catttctaaa atggcagctt cagttctaga    5100
gaagaaagaa caacatcagc agtaaagtcc atggaatagc tagtggtctg tgtttctttt    5160
cgccattgcc tagcttgccg taatgattct ataatgccat catgcagcaa ttatgagagg    5220
ctaggtcatc caaagagaag accctatcaa tgtaggttgc aaaatctaac ccctaaggaa    5280
gtgcagtctt tgatttgatt tccctagtaa ccttgcagat atgtttaacc aagccatagc    5340
ccatgccttt tgagggctga acaaataagg gacttactga taatttactt ttgatcacat    5400
taaggtgttc tcaccttgaa atcttataca ctgaaatggc cattgattta ggccactggc    5460
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aattatgaga tggactgtgg gtactgggag tgatcactaa caccatagta atgtctaata    5580
ttcacaggca gatctgcttg gggaagctag ttatgtgaaa ggcaaataaa gtcatacagt    5640
agctcaaaag gcaaccataa ttctctttgg tgcaagtctt gggagcgtga tctagattac    5700
actgcaccat tcccaagtta atcccctgaa aacttactct caactggagc aaatgaactt    5760
tggtcccaaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc    5820
ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta    5880
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tctattcatt tttttgcatc caattgtgcc tgaactttta aaatatgtaa atgctgccat    6000
gttccaaacc catcgtcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt    6060
gtcccatgag caggtgcctg agacacagac cccttttgcat tcacagagag gtcattggtt   6120
atagagactt gaattaataa gtgacattat gccagttct gttctctcac aggtgataaa     6180
caatgctttt tgtgcactac atactcttca gtgtagagct cttgtttat gggaaaaggc      6240
tcaaatgcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact    6300
gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct    6360
tttgcacttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac    6420
ctatttgatg ttcaaataaa gaattaaact                                      6450
```

```
<210> 26
<211> 614
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 26
Met Asn Thr Phe Gln Asp Gln Ser Gly Ser Ser Ser Asn Arg Glu Pro
1               5                   10                  15
Leu Leu Arg Cys Ser Asp Ala Arg Arg Asp Leu Glu Leu Ala Ile Gly
            20                  25                  30
Gly Val Leu Arg Ala Glu Gln Gln Ile Lys Asp Asn Leu Arg Glu Val
        35                  40                  45
```

```
Lys Ala Gln Ile His Ser Cys Ile Ser Arg His Leu Glu Cys Leu Arg
    50              55              60
Ser Arg Glu Val Trp Leu Tyr Glu Gln Val Asp Leu Ile Tyr Gln Leu
65              70              75              80
Lys Glu Glu Thr Leu Gln Gln Gln Ala Gln Gln Leu Tyr Ser Leu Leu
            85              90              95
Gly Gln Phe Asn Cys Leu Thr His Gln Leu Glu Cys Thr Gln Asn Lys
            100             105             110
Asp Leu Ala Asn Gln Val Ser Val Cys Leu Glu Arg Leu Gly Ser Leu
    115             120             125
Thr Leu Lys Pro Glu Asp Ser Thr Val Leu Leu Phe Glu Ala Asp Thr
    130             135             140
Ile Thr Leu Arg Gln Thr Ile Thr Thr Phe Gly Ser Leu Lys Thr Ile
145             150             155             160
Gln Ile Pro Glu His Leu Met Ala His Ala Ser Ser Ala Asn Ile Gly
            165             170             175
Pro Phe Leu Glu Lys Arg Gly Cys Ile Ser Met Pro Glu Gln Lys Ser
            180             185             190
Ala Ser Gly Ile Val Ala Val Pro Phe Ser Glu Trp Leu Leu Gly Ser
            195             200             205
Lys Pro Ala Ser Gly Tyr Gln Ala Pro Tyr Ile Pro Ser Thr Asp Pro
    210             215             220
Gln Asp Trp Leu Thr Gln Lys Gln Thr Leu Glu Asn Ser Gln Thr Ser
225             230             235             240
Ser Arg Ala Cys Asn Phe Phe Asn Asn Val Gly Gly Asn Leu Lys Gly
            245             250             255
Leu Glu Asn Trp Leu Leu Lys Ser Glu Lys Ser Ser Tyr Gln Lys Cys
            260             265             270
Asn Ser His Ser Thr Thr Ser Ser Phe Ser Ile Glu Met Glu Lys Val
    275             280             285
Gly Asp Gln Glu Leu Pro Asp Gln Asp Glu Met Asp Leu Ser Asp Trp
    290             295             300
Leu Val Thr Pro Gln Glu Ser His Lys Leu Arg Lys Pro Glu Asn Gly
305             310             315             320
Ser Arg Glu Thr Ser Glu Lys Phe Lys Leu Leu Phe Gln Ser Tyr Asn
            325             330             335
Val Asn Asp Trp Leu Val Lys Thr Asp Ser Cys Thr Asn Cys Gln Gly
            340             345             350
Asn Gln Pro Lys Gly Val Glu Ile Glu Asn Leu Gly Asn Leu Lys Cys
    355             360             365
Leu Asn Asp His Leu Glu Ala Lys Lys Pro Leu Ser Thr Pro Ser Met
    370             375             380
Val Thr Glu Asp Trp Leu Val Gln Asn His Gln Asp Pro Cys Lys Val
385             390             395             400
Glu Glu Val Cys Arg Ala Asn Glu Pro Cys Thr Ser Phe Ala Glu Cys
            405             410             415
Val Cys Asp Glu Asn Cys Glu Lys Glu Ala Leu Tyr Lys Trp Leu Leu
            420             425             430
Lys Lys Glu Gly Lys Asp Lys Asn Gly Met Pro Val Glu Pro Lys Pro
            435             440             445
Glu Pro Glu Lys His Lys Asp Ser Leu Asn Met Trp Leu Cys Pro Arg
    450             455             460
Lys Glu Val Ile Glu Gln Thr Lys Ala Pro Lys Ala Met Thr Pro Ser
465             470             475             480
Arg Ile Ala Asp Ser Phe Gln Val Ile Lys Asn Ser Pro Leu Ser Glu
            485             490             495
Trp Leu Ile Arg Pro Pro Tyr Lys Glu Gly Ser Pro Lys Glu Val Pro
            500             505             510
Gly Thr Glu Asp Arg Ala Gly Lys Gln Lys Phe Lys Ser Pro Met Asn
            515             520             525
```

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```
Thr Ser Trp Cys Ser Phe Asn Thr Ala Asp Trp Val Leu Pro Gly Lys
    530                 535                 540
Lys Met Gly Asn Leu Ser Gln Leu Ser Ser Gly Glu Asp Lys Trp Leu
545                 550                 555                 560
Leu Arg Lys Lys Ala Gln Glu Val Leu Leu Asn Ser Pro Leu Gln Glu
                565                 570                 575
Glu His Asn Phe Pro Pro Asp His Tyr Gly Leu Pro Ala Val Cys Asp
                580                 585                 590
Leu Phe Ala Cys Met Gln Leu Lys Val Asp Lys Glu Lys Trp Leu Tyr
        595                 600                 605
Arg Thr Pro Leu Gln Met
    610
```

<210> 27
<211> 1845
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 27

```
atgaatacct tccaagacca gagtggcagc tccagtaata gagaacccct tttgaggtgt      60
agtgatgcac ggagggactt ggagcttgct attggtggag ttctccgggc tgaacagcaa     120
attaaagata acttgcgaga ggtcaaagct cagattcaca gttgcataag ccgtcacctg     180
gaatgtctta gaagccgtga ggtatggctg tatgaacagg tggaccttat ttatcagctt     240
aaagaggaga cacttcaaca gcaggctcag cagctctact cgttattggg ccagttcaat     300
tgtcttactc atcaactgga gtgtacccaa aacaaagatc tagccaatca agtctctgtg     360
tgcctggaga dactgggcag tttgacccttt aagcctgaag attcaactgt cctgctcttt     420
gaagctgaca caattactct gcgccagacc atcaccacat ttgggtctct caaaaccatt     480
caaattcctg agcacttgat ggctcatgct agttcagcaa atattgggcc cttcctggag     540
aagagaggct gtatctccat gccagagcag aagtcagcat ccggtattgt agctgtccct     600
ttcagcgaat ggctccttgg aagcaaacct gccagtggtt atcaagctcc ttacataccc     660
agcaccgacc cccaggactg gcttacccaa aagcagacct ggagaacag tcagacttct     720
tccagagcct gcaatttctt caataatgtc gggggaaacc taaagggctt agaaaactgg     780
ctcctcaaga gtgaaaaatc aagttatcaa aagtgtaaca gccattccac tactagttct     840
ttctccattg aaatggaaaa ggttggagat caagagcttc ctgatcaaga tgagatggac     900
ctatcagatt ggctagtgac tccccaggaa tcccataagc tgcggaagcc tgagaatggc     960
agtcgtgaaa ccagtgagaa gtttaagctc ttattccagt cctataatgt gaatgattgg    1020
cttgtcaaga ctgactcctg taccaactgt cagggaaacc agcccaaagg tgtggagatt    1080
gaaaacctgg gcaatctgaa gtgcctgaat gaccacttgg aggccaagaa accattgtcc    1140
accccccagca tggttacaga ggattggctt gtccagaacc atcaggaccc atgtaaggta    1200
gaggaggtgt gcagagccaa tgagccctgc acaagctttg cagagtgtgt gtgtgatgag    1260
aattgtgaga aggaggctct gtataagtgg cttctgaaga aagaaggaaa ggataaaaat    1320
gggatgcctg tggaacccaa acctgagcct gagaagcata agattccct gaatatgtgg    1380
ctctgtccta gaaaagaagt aatagaacaa actaaagcac caaaggcaat gactccttct    1440
agaattgctg attccttcca agtcataaag aacagcccct gtcggagtg gcttatcagg    1500
ccccccataca aagaaggaag tcccaaggaa gtgcctggta ctgaagacag agctggcaaa    1560
cagaagttta aaagccccat gaatacttcc tggtgttcct ttaacacagc tgactgggtc    1620
ctgccaggaa agaagatggg caacctcagc cagttatctt ctggagaaga caagtggctg    1680
cttcgaaaga aggcccagga agtattactt aattcacctc tacaggagga acataacttc    1740
cccccagacc attatggcct ccctgcagtt tgtgatctct ttgcctgtat gcagcttaaa    1800
gttgataaag agaagtggtt atatcgaact cctctacaga tgtga                    1845
```

<210> 28
<211> 474
<212> PRT
<213> Artificial Sequence

<220>

37

<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 28
```
Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
 1               5                  10                  15
Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
                20                  25                  30
Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
            35                  40                  45
Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
        50                  55                  60
Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
65                  70                  75                  80
Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
                85                  90                  95
Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
            100                 105                 110
Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
        115                 120                 125
Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe
    130                 135                 140
Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln
145                 150                 155                 160
Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp
                165                 170                 175
Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu
            180                 185                 190
Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln
        195                 200                 205
Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe
    210                 215                 220
Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His
225                 230                 235                 240
Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg
                245                 250                 255
Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser
            260                 265                 270
Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe
        275                 280                 285
Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala
    290                 295                 300
Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln
305                 310                 315                 320
Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe
                325                 330                 335
Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val
            340                 345                 350
Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp
        355                 360                 365
Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile
    370                 375                 380
Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn
385                 390                 395                 400
Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly
                405                 410                 415
Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile
            420                 425                 430
Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
        435                 440                 445
```

```
Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
    450             455             460
Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
465                 470
```

<210> 29
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 29
```
ggtctctggt ctcccctctc tgagcactct gaggtcctta tgtcgtcaga agatcgagaa      60
gctcaggagg atgaattgct ggccctggca agtatttacg atggagatga atttagaaaa     120
gcagagtctg tccaaggtgg agaaaccagg atctatttgg atttgccaca gaatttcaag     180
atatttgtga gcggcaattc aaatgagtgt ctccagaata gtggctttga atacaccatt     240
tgctttctgc ctccacttgt gctgaacttt gaactgccac cagattatcc atcctcttcc     300
ccaccttcat tcacacttag tggcaaatgg ctgtcaccaa ctcagctatc tgctctatgc     360
aagcacttag acaacctatg ggaagaacac cgtggcagcg tggtcctgtt tgcctggatg     420
caatttctta aggaagagac cctagcatac ttgaatattg tctctccttt tgagctcaag     480
attggttctc agaaaaaagt gcagagaagg acagctcaag cttctcccaa cacagagcta     540
gattttggag gagctgctgg atctgatgta gaccaagagg aaattgtgga tgagagagca     600
gtgcaggatg tggaatcact gtcaaatctg atccaggaaa tcttggactt tgatcaagct     660

cagcagataa aatgctttaa tagtaaattg ttcctgtgca gtatctgttt ctgtgagaag     720
ctgggtagtg aatgcatgta cttcttggag tgcaggcatg tgtactgcaa agcctgtctg     780
aaggactact ttgaaatcca gatcagagat ggccaggttc aatgcctcaa ctgcccagaa     840
ccaaagtgcc cttcggtggc cactcctggt caggtcaaag agttagtgga agcagagtta     900
tttgcccgtt atgaccgcct tctcctccag tcctccttgg acctgatggc agatgtggtg     960
tactgccccc ggccgtgctg ccagctgcct gtgatgcagg aacctggctg caccatgggt    1020
atctgctcca gctgcaattt tgccttctgt actttgtgca ggttgaccta ccatgggtc     1080
tccccatgta aggtgactgc agagaaatta atggacttac gaaatgaata cctgcaagcg    1140
gatgaggcta ataaaagact tttggatcaa aggtatggta agagagtgat tcagaaggca    1200
ctggaagaga tggaaagtaa ggagtggcta gagaagaact caaagagctg cccatgttgt    1260
ggaactccca tagagaaatt agacggatgt aacaagatga catgtactgg ctgtatgcaa    1320
tatttctgtt ggatttgcat gggttctctc tctagagcaa acccttacaa acatttcaat    1380
gaccctggtt caccatgttt taaccggctg ttttatgctg tggatgttga cgacgatatt    1440
tgggaagatg aggtagaaga ctagttaact actgctcaag atatggaagt ggattgtttt    1500
tccctaatct tccgtcaagt acacaaagta actttgcggg atatttaggg tactattcat    1560
tcactcttcc tgcgtagaag atatggaaga acgaggttta tattttcatg tggtactact    1620
gaagaaggtg cattgataca tttttaaatg taagttgaga aaaatttata agccaaggt     1680
tcagaaaatt aaactacaga a                                              1701
```

<210> 30
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 30
```
Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
 1               5                  10                  15
Pro Pro Pro Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser
                20                  25                  30
```

```
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
        35              40              45
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
    50              55              60
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
65              70              75              80
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
            85              90              95
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
        100             105             110
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
        115             120             125
Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
    130             135             140
Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145             150             155             160
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
            165             170             175
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
        180             185             190
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
        195             200             205
Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
    210             215             220
Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225             230             235             240
Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
            245             250             255
Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
            260             265             270
Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
    275             280             285
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
    290             295             300
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305             310             315             320
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
            325             330             335
Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys
            340             345             350
Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe
            355             360             365
Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg
    370             375             380
Gly Ser Leu Trp Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val
385             390             395             400
Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe
            405             410             415
Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys
        420             425             430
Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly
        435             440
```

<210> 31
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
    synthetic construct

<400> 31

```
atgccaaggt caggggctcc caaagagcgc cctgcggagc ctctcacccc tcccccatcc        60

tatggccacc agccacagac agggtctggg gagtcttcag gagcctcggg ggacaaggac       120
cacctgtaca gcacggtatg caagcctcgg tccccaaagc ctgcagcccc ggccgcccct       180
ccattctcct cttccagcgg tgtcttgggt accgggctct gtgagctaga tcggttgctt       240
caggaactta atgccactca gttcaacatc acagatgaaa tcatgtctca gttcccatct       300
agcaaggtgg cttcaggaga gcagaaggag gaccagtctg aagataagaa aagacccagc       360
ctcccttcca gcccgtctcc tggcctccca aaggcttctg ccacctcagc cactctggag       420
ctggatagac tgatggcctc actccctgac ttccgcgttc aaaaccatct tccagcctct       480
gggccaactc agccaccggt ggtgagctcc acaaatgagg ctcccccatc cccaccagag       540
ccgactgcaa agggcagcct agacaccatg ctggggctgc tgcagtccga cctcagccgc       600
cggggtgttc ccacccaggc caaaggcctc tgtggctcct gcaataaacc tattgctggg       660
caagtggtga cggctctggg ccgcgcctgg caccccgagc acttcgtttg cggaggctgt       720
tccaccgccc tgggaggcag cagcttcttc gagaaggatg agcccccctt ctgccccgag       780
tgctactttg agcgcttctc gccaagatgt ggcttctgca accagcccat ccgacacaag       840
atggtgaccg ccttgggcac tcactggcac ccagagcatt tctgctgcgt cagttgcggg       900
gagcccttcg agatgaggg tttccacgag cgcgagggcc gcccctactg ccgccgggac       960
ttcctgcagc tgttcgcccc gcgctgccag ggctgccagg ccccatcct ggataactac      1020
atctcggcgc tcagcctgct ctggcacccg gactgtttcg tctgcaggga atgcttcgcg      1080
cccttctcgg gaggcagctt tttcgagcac gagggccgcc gttgtgcga gaaccacttc      1140
cacgcacgac gcggctcgct gtggcccacg tgtggcctcc ctgtgaccgg ccgctgcgtg      1200
tcggccctgg tcgccgctt ccacccggac cacttcgcat gcaccttctg cctgcgcccg      1260
ctcaccaagg ggtccttcca ggagcgcgcc ggcaagccct actgccagcc ctgcttcctg      1320
aagctcttcg gctga                                                        1335
```

<210> 32
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 32

```
Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
1               5                   10                  15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
                20                  25                  30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
            35                  40                  45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
        50                  55                  60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65                  70                  75                  80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
                85                  90                  95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
                100                 105                 110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
            115                 120                 125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
        130                 135                 140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145                 150                 155                 160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
                165                 170                 175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
                180                 185                 190
```

```
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
        195             200             205
Leu Pro Asp Glu Asp Asp Asp Leu
    210             215
```

<210> 33
<211> 1566
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 33
```
ggcgcttctg gaaggaacgc cgcgatggct gcgcagggag agccccaggt ccagttcaaa      60
cttgtattgg ttggtgatgg tggtactgga aaaacgacct tcgtgaaacg tcatttgact     120
ggtgaatttg agaagaagta tgtagccacc ttgggtgttg aggttcatcc cctagtgttc     180
cacaccaaca gaggacctat taagttcaat gtatgggaca cagccggcca ggagaaattc     240
ggtggactga gagatggcta ttatatccaa gcccagtgtg ccatcataat gtttgatgta     300
acatcgagag ttacttacaa gaatgtgcct aactggcata gagatctggt acgagtgtgt     360
gaaaacatcc ccattgtgtt gtgtggcaac aaagtggata ttaaggacag gaaagtgaag     420
gcgaaatcca ttgtcttcca ccgaaagaag aatcttcagt actacgacat ttctgccaaa     480
agtaactaca actttgaaaa gcccttcctc tggcttgcta ggaagctcat tggagaccct     540
aacttggaat ttgttgccat gcctgctctc gccccaccag aagttgtcat ggacccagct     600
ttggcagcac agtatgagca cgacttagag gttgctcaga caactgctct cccggatgag     660
gatgatgacc tgtgagaatg aagctggagc ccagcgtcag aagtctagtt ttataggcag     720
ctgtcctgtg atgtcagcgg tgcagcgtgt gtgccacctc attattatct agctaagcgg     780
aacatgtgct ttatctgtgg gatgctgaag gagatgagtg ggcttcggag tgaatgtggc     840
agtttaaaaa ataacttcat tgtttggacc tgcatattta gctgtttgga cgcagttgat     900
tccttgagtt tcatatataa gactgctgca gtcacatcac aatattcagt ggtgaaatct     960
tgtttgttac tgtcattccc attccttttc tttagaatca gaataaagtt gtatttcaaa    1020
tatctaagca agtgaactca tcccttgttt ataaatagca tttggaaacc actaaagtag    1080
ggaagtttta tgccatgtta atatttgaat tgccttgctt ttatcactta atttgaaatc    1140
tattgggtta atttctccct atgtttattt ttgtacattt gagccatgtc acacaaactg    1200
atgatgacag gtcagcagta ttctatttgg ttagaagggt tacatggtgt aaatattagt    1260
gcagttaagc taaagcagtg tttgctccac cttcatattg gctaggtagg gtcacctagg    1320
gaagcacttg ctcaaaatct gtgacctgtc agaataaaaa tgtggtttgt acatatcaaa    1380
tagatatttt aagggtaata ttttctttta tggcaaaagt aatcatgttt taatgtagaa    1440
cctcaaacag gatggaacat cagtggatgg caggaggttg ggaattcttg ctgttaaaaa    1500
taattacaaa ttttgcactt tttgtttgaa tgttagatgc ttagtgtgaa gttgatacgc    1560
aagccg                                                               1566
```

<210> 34
<211> 2427
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 34
```
Met Pro Leu Lys Thr Arg Thr Ala Leu Ser Asp Asp Pro Asp Ser Ser
 1               5              10             15
Thr Ser Thr Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser
            20             25             30
Ser Thr Ser Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr
        35             40             45
Pro Leu Lys Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg
    50             55             60
```

```
Arg Pro Trp Trp Pro Cys Arg Ile Cys Ser Asp Pro Leu Ile Asn Thr
65              70              75
His Ser Lys Met Lys Val Ser Asn Arg Arg Pro Tyr Arg Gln Tyr Tyr
            85              90              95
Val Glu Ala Phe Gly Asp Pro Ser Glu Arg Ala Trp Val Ala Gly Lys
            100             105             110
Ala Ile Val Met Phe Glu Gly Arg His Gln Phe Glu Glu Leu Pro Val
            115             120             125
Leu Arg Arg Arg Gly Lys Gln Lys Glu Lys Gly Tyr Arg His Lys Val
    130             135             140
Pro Gln Lys Ile Leu Ser Lys Trp Glu Ala Ser Val Gly Leu Ala Glu
145             150             155             160
Gln Tyr Asp Val Pro Lys Gly Ser Lys Asn Arg Lys Cys Ile Pro Gly
            165             170             175
Ser Ile Lys Leu Asp Ser Glu Glu Asp Met Pro Phe Glu Asp Cys Thr
            180             185             190
Asn Asp Pro Glu Ser Glu His Asp Leu Leu Leu Asn Gly Cys Leu Lys
            195             200             205
Ser Leu Ala Phe Asp Ser Glu His Ser Ala Asp Glu Lys Glu Lys Pro
    210             215             220
Cys Ala Lys Ser Arg Ala Arg Lys Ser Ser Asp Asn Pro Lys Arg Thr
225             230             235             240
Ser Val Lys Lys Gly His Ile Gln Phe Glu Ala His Lys Asp Glu Arg
            245             250             255
Arg Gly Lys Ile Pro Glu Asn Leu Gly Leu Asn Phe Ile Ser Gly Asp
            260             265             270
Ile Ser Asp Thr Gln Ala Ser Asn Glu Leu Ser Arg Ile Ala Asn Ser

    275             280             285
Leu Thr Gly Ser Asn Thr Ala Pro Gly Ser Phe Leu Phe Ser Ser Cys
    290             295             300
Gly Lys Asn Thr Ala Lys Lys Glu Phe Glu Thr Ser Asn Gly Asp Ser
305             310             315             320
Leu Leu Gly Leu Pro Glu Gly Ala Leu Ile Ser Lys Cys Ser Arg Glu
            325             330             335
Lys Asn Lys Pro Gln Arg Ser Leu Val Cys Gly Ser Lys Val Lys Leu
            340             345             350
Cys Tyr Ile Gly Ala Gly Asp Glu Glu Lys Arg Ser Asp Ser Ile Ser
            355             360             365
Ile Cys Thr Thr Ser Asp Asp Gly Ser Ser Asp Leu Asp Pro Ile Glu
    370             375             380
His Ser Ser Glu Ser Asp Asn Ser Val Leu Glu Ile Pro Asp Ala Phe
385             390             395             400
Asp Arg Thr Glu Asn Met Leu Ser Met Gln Lys Asn Glu Lys Ile Lys
            405             410             415
Tyr Ser Arg Phe Ala Ala Thr Asn Thr Arg Val Lys Ala Lys Gln Lys
            420             425             430
Pro Leu Ile Ser Asn Ser His Thr Asp His Leu Met Gly Cys Thr Lys
            435             440             445
Ser Ala Glu Pro Gly Thr Glu Thr Ser Gln Val Asn Leu Ser Asp Leu
    450             455             460
Lys Ala Ser Thr Leu Val His Lys Pro Gln Ser Asp Phe Thr Asn Asp
465             470             475             480
Ala Leu Ser Pro Lys Phe Asn Leu Ser Ser Ser Ile Ser Ser Glu Asn
            485             490             495
Ser Leu Ile Lys Gly Gly Ala Ala Asn Gln Ala Leu Leu His Ser Lys
            500             505             510
Ser Lys Gln Pro Lys Phe Arg Ser Ile Lys Cys Lys His Lys Glu Asn
            515             520             525
Pro Val Met Ala Glu Pro Pro Val Ile Asn Glu Glu Cys Ser Leu Lys
    530             535             540
```

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```
Cys Cys Ser Ser Asp Thr Lys Gly Ser Pro Leu Ala Ser Ile Ser Lys
545             550             555                     560
Ser Gly Lys Val Asp Gly Leu Lys Leu Leu Asn Asn Met His Glu Lys
                565             570                 575
Thr Arg Asp Ser Ser Asp Ile Glu Thr Ala Val Val Lys His Val Leu
            580             585                 590
Ser Glu Leu Lys Glu Leu Ser Tyr Arg Ser Leu Gly Glu Asp Val Ser
        595             600                 605
Asp Ser Gly Thr Ser Lys Pro Ser Lys Pro Leu Leu Phe Ser Ser Ala
    610             615             620
Ser Ser Gln Asn His Ile Pro Ile Glu Pro Asp Tyr Lys Phe Ser Thr
625             630             635                     640
Leu Leu Met Met Leu Lys Asp Met His Asp Ser Lys Thr Lys Glu Gln
            645             650                 655
Arg Leu Met Thr Ala Gln Asn Leu Val Ser Tyr Arg Ser Pro Gly Arg
            660             665             670
Gly Asp Cys Ser Thr Asn Ser Pro Val Gly Val Ser Lys Val Leu Val
        675             680             685
Ser Gly Gly Ser Thr His Asn Ser Glu Lys Lys Gly Asp Gly Thr Gln
    690             695             700
Asn Ser Ala Asn Pro Ser Pro Ser Gly Gly Asp Ser Ala Leu Ser Gly
705             710             715                     720
Glu Leu Ser Ala Ser Leu Pro Gly Leu Leu Ser Asp Lys Arg Asp Leu
            725             730                 735
Pro Ala Ser Gly Lys Ser Arg Ser Asp Cys Val Thr Arg Arg Asn Cys
            740             745                 750
Gly Arg Ser Lys Pro Ser Ser Lys Leu Arg Asp Ala Phe Ser Ala Gln
        755             760             765
Met Val Lys Asn Thr Val Asn Arg Lys Ala Leu Lys Thr Glu Arg Lys
    770             775             780
Arg Lys Leu Asn Gln Leu Pro Ser Val Thr Leu Asp Ala Val Leu Gln
785             790             795                     800
Gly Asp Arg Glu Arg Gly Gly Ser Leu Arg Gly Gly Ala Glu Asp Pro
            805             810                 815
Ser Lys Glu Asp Pro Leu Gln Ile Met Gly His Leu Thr Ser Glu Asp
        820             825             830
Gly Asp His Phe Ser Asp Val His Phe Asp Ser Lys Val Lys Gln Ser
        835             840             845
Asp Pro Gly Lys Ile Ser Glu Lys Gly Leu Ser Phe Glu Asn Gly Lys
    850             855             860
Gly Pro Glu Leu Asp Ser Val Met Asn Ser Glu Asn Asp Glu Leu Asn
865             870             875                     880
Gly Val Asn Gln Val Val Pro Lys Lys Arg Trp Gln Arg Leu Asn Gln
            885             890                 895
Arg Arg Thr Lys Pro Arg Lys Arg Met Asn Arg Phe Lys Glu Lys Glu
            900             905                 910
Asn Ser Glu Cys Ala Phe Arg Val Leu Leu Pro Ser Asp Pro Val Gln
        915             920             925
Glu Gly Arg Asp Glu Phe Pro Glu His Arg Thr Pro Ser Ala Ser Ile
    930             935             940
Leu Glu Glu Pro Leu Thr Glu Gln Asn His Ala Asp Cys Leu Asp Ser
945             950             955                     960
Ala Gly Pro Arg Leu Asn Val Cys Asp Lys Ser Ser Ala Ser Ile Gly
            965             970                 975
Asp Met Glu Lys Glu Pro Gly Ile Pro Ser Leu Thr Pro Gln Ala Glu
        980             985             990
Leu Pro Glu Pro Ala Val Arg Ser Glu Lys Lys Arg Leu Arg Lys Pro
        995             1000            1005
Ser Lys Trp Leu Leu Glu Tyr Thr Glu Glu Tyr Asp Gln Ile Phe Ala
    1010            1015            1020
```

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```
Pro Lys Lys Lys Gln Lys Lys Val Gln Glu Gln Val His Lys Val Ser
1025             1030             1035             1040
Ser Arg Cys Glu Glu Glu Ser Leu Leu Ala Arg Gly Arg Ser Ser Ala
                1045             1050             1055
Gln Asn Lys Gln Val Asp Glu Asn Ser Leu Ile Ser Thr Lys Glu Glu
            1060             1065             1070
Pro Pro Val Leu Glu Arg Glu Ala Pro Phe Leu Glu Gly Pro Leu Ala
            1075             1080             1085
Gln Ser Glu Leu Gly Gly Gly His Ala Glu Leu Pro Gln Leu Thr Leu
            1090             1095             1100
Ser Val Pro Val Ala Pro Glu Val Ser Pro Arg Pro Ala Leu Glu Ser
1105             1110             1115             1120
Glu Glu Leu Leu Val Lys Thr Pro Gly Asn Tyr Glu Ser Lys Arg Gln
                1125             1130             1135
Arg Lys Pro Thr Lys Lys Leu Leu Glu Ser Asn Asp Leu Asp Pro Gly
            1140             1145             1150
Phe Met Pro Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu
            1155             1160             1165
Ala Gly His Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr
            1170             1175             1180
Ser Lys Asp Phe Gly Gly Gly Thr Thr Lys Ile Phe Asp Lys Pro Arg
1185             1190             1195             1200
Lys Arg Lys Arg Gln Arg His Ala Ala Ala Lys Met Gln Cys Lys Lys
                1205             1210             1215
Val Lys Asn Asp Asp Ser Ser Lys Glu Ile Pro Gly Ser Glu Gly Glu
                1220             1225             1230
Leu Met Pro His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu
            1235             1240             1245
Gly Val Glu His Asp Pro Gly Met Pro Ala Ser Lys Lys Met Gln Gly
            1250             1255             1260
Glu Arg Gly Gly Gly Ala Ala Leu Lys Glu Asn Val Cys Gln Asn Cys
1265             1270             1275             1280
Glu Lys Leu Gly Glu Leu Leu Leu Cys Glu Ala Gln Cys Cys Gly Ala
                1285             1290             1295
Phe His Leu Glu Cys Leu Gly Leu Thr Glu Met Pro Arg Gly Lys Phe
                1300             1305             1310
Ile Cys Asn Glu Cys Arg Thr Gly Ile His Thr Cys Phe Val Cys Lys
                1315             1320             1325
Gln Ser Gly Glu Asp Val Lys Arg Cys Leu Leu Pro Leu Cys Gly Lys
            1330             1335             1340
Phe Tyr His Glu Glu Cys Val Gln Lys Tyr Pro Pro Thr Val Met Gln
1345             1350             1355             1360
Asn Lys Gly Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala
                1365             1370             1375
Ala Asn Pro Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys
            1380             1385             1390
Val Arg Cys Pro Val Ala Tyr His Ala Asn Asp Phe Cys Leu Ala Ala
            1395             1400             1405
Gly Ser Lys Ile Leu Ala Ser Asn Ser Ile Ile Cys Pro Asn His Phe
            1410             1415             1420
Thr Pro Arg Arg Gly Cys Arg Asn His Glu His Val Asn Val Ser Trp
1425             1430             1435             1440
Cys Phe Val Cys Ser Glu Gly Gly Ser Leu Leu Cys Cys Asp Ser Cys
                1445             1450             1455
Pro Ala Ala Phe His Arg Glu Cys Leu Asn Ile Asp Ile Pro Glu Gly
            1460             1465             1470
Asn Trp Tyr Cys Asn Asp Cys Lys Ala Gly Lys Lys Pro His Tyr Arg
            1475             1480             1485
Glu Ile Val Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu
            1490             1495             1500
```

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Ile Cys His Pro Arg Ala Val Pro Ser Asn Ile Asp Lys Met Arg His
1505   1510   1515   1520
Asp Val Gly Glu Phe Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu
                1525   1530   1535
Trp Thr His Gln Ala Arg Val Phe Pro Tyr Met Glu Gly Asp Val Ser
                1540   1545   1550
Ser Lys Asp Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala
                1555   1560   1565
Leu Gln Glu Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu
        1570   1575   1580
Leu Arg Gln Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro
1585   1590   1595   1600
Tyr Lys His Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe
                1605   1610   1615
Thr Ala Asp Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp
                1620   1625   1630
Glu Asn Pro Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu
                1635   1640   1645
Tyr Glu Cys His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn
        1650   1655   1660
Gln Cys Phe Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr
1665   1670   1675   1680
Leu Gln Arg Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly
                1685   1690   1695
Glu Phe Val Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys
                1700   1705   1710
Arg Ala Arg Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr
        1715   1720   1725
Met Leu Thr Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly
        1730   1735   1740
Asn Tyr Ala Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr
1745   1750   1755   1760
Gln Lys Trp Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu
                1765   1770   1775
Ser Asp Ile Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu
                1780   1785   1790
Cys Leu Gly Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys
                1795   1800   1805
Ser Gly Phe Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu
        1810   1815   1820
Glu Lys Ser Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr
1825   1830   1835   1840
Gln Gly Glu Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly
                1845   1850   1855
Asp Ala Gly Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val
                1860   1865   1870
Tyr His Ala Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp
        1875   1880   1885
Glu Cys Pro Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser
        1890   1895   1900
Phe Cys Glu Met Cys Pro Ser Ser Phe Cys Lys Gln His Arg Glu Gly
1905   1910   1915   1920
Met Leu Phe Ile Ser Lys Leu Asp Gly Arg Leu Ser Cys Thr Glu His
                1925   1930   1935
Asp Pro Cys Gly Pro Asn Pro Leu Glu Pro Gly Glu Ile Arg Glu Tyr
        1940   1945   1950
Val Pro Pro Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala
        1955   1960   1965
Glu Gln Ser Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys
        1970   1975   1980

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```
Pro Pro Ala Asp Thr Asn Gln Met Leu Ser Leu Ser Lys Lys Ala Leu
1985                1990            1995            2000
Ala Gly Thr Cys Gln Arg Pro Leu Leu Pro Glu Arg Pro Leu Glu Arg
                2005            2010            2015
Thr Asp Ser Arg Pro Gln Pro Leu Asp Lys Val Arg Asp Leu Ala Gly
            2020            2025            2030
Ser Gly Thr Lys Ser Gln Ser Leu Val Ser Ser Gln Arg Pro Leu Asp
            2035            2040            2045
Arg Pro Pro Ala Val Ala Gly Pro Arg Pro Gln Leu Ser Asp Lys Pro
    2050            2055            2060
Ser Pro Val Thr Ser Pro Ser Ser Ser Pro Ser Val Arg Ser Gln Pro
2065            2070            2075            2080
Leu Glu Arg Pro Leu Gly Thr Ala Asp Pro Arg Leu Asp Lys Ser Ile
            2085            2090            2095
Gly Ala Ala Ser Pro Arg Pro Gln Ser Leu Glu Lys Thr Ser Val Pro
            2100            2105            2110
Thr Gly Leu Arg Leu Pro Pro Pro Asp Arg Leu Leu Ile Thr Ser Ser
            2115            2120            2125
Pro Lys Pro Gln Thr Ser Asp Arg Pro Thr Asp Lys Pro His Ala Ser
    2130            2135            2140
Leu Ser Gln Arg Leu Pro Pro Pro Glu Lys Val Leu Ser Ala Val Val
2145            2150            2155            2160
Gln Thr Leu Val Ala Lys Glu Lys Ala Leu Arg Pro Val Asp Gln Asn
            2165            2170            2175
Thr Gln Ser Lys Asn Arg Ala Ala Leu Val Met Asp Leu Ile Asp Leu

            2180            2185            2190
Thr Pro Arg Gln Lys Glu Arg Ala Ala Ser Pro His Gln Val Thr Pro
    2195            2200            2205
Gln Ala Asp Glu Lys Met Pro Val Leu Glu Ser Ser Ser Trp Pro Ala
    2210            2215            2220
Ser Lys Gly Leu Gly His Met Pro Arg Ala Val Glu Lys Gly Cys Val
2225            2230            2235            2240
Ser Asp Pro Leu Gln Thr Ser Gly Lys Ala Ala Ala Pro Ser Glu Asp
            2245            2250            2255
Pro Trp Gln Ala Val Lys Ser Leu Thr Gln Ala Arg Leu Leu Ser Gln
            2260            2265            2270
Pro Pro Ala Lys Ala Phe Leu Tyr Glu Pro Thr Thr Gln Ala Ser Gly
    2275            2280            2285
Arg Ala Ser Ala Gly Ala Glu Gln Thr Pro Gly Pro Leu Ser Gln Ser
    2290            2295            2300
Pro Gly Leu Val Lys Gln Ala Lys Gln Met Val Gly Gly Gln Gln Leu
2305            2310            2315            2320
Pro Ala Leu Ala Ala Lys Ser Gly Gln Ser Phe Arg Ser Leu Gly Lys
            2325            2330            2335
Ala Pro Ala Ser Leu Pro Thr Glu Glu Lys Lys Leu Val Thr Thr Glu
            2340            2345            2350
Gln Ser Pro Trp Ala Leu Gly Lys Ala Ser Ser Arg Ala Gly Leu Trp
            2355            2360            2365
Pro Ile Val Ala Gly Gln Thr Leu Ala Gln Ser Cys Trp Ser Ala Gly
    2370            2375            2380
Ser Thr Gln Thr Leu Ala Gln Thr Cys Trp Ser Leu Gly Arg Gly Gln
2385            2390            2395            2400
Asp Pro Lys Pro Glu Gln Asn Thr Leu Pro Ala Leu Asn Gln Ala Pro
            2405            2410            2415
Ser Ser His Lys Cys Ala Glu Ser Glu Gln Lys
            2420            2425
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<210> 35
<211> 7707
<212> DNA
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 35
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cagcccttttc ggatgatcca gattccagta ccagtacatt aggaaacatg ctagaattac      180
ctggaacttc atcatcatct acttcacagg aattgccatt ttgtcaacct aagaaaaagt      240
ctacgccact gaagtatgaa gttggagatc tcatctgggc aaaattcaag agacgcccat      300
ggtggccctg caggatttgt tctgatccgt tgattaacac acattcaaaa atgaaagttt      360
ccaaccggag gccctatcgg cagtactacg tggaggcttt tggagatcct tctgagagag      420
cctgggtggc tggaaaagca atcgtcatgt ttgaaggcag acatcaattc gaagagctac      480
ctgtccttag gagaagaggg aaacagaaag aaaaaggata taggcataag gttcctcaga      540
aaattttgag taaatgggaa gccagtgttg gacttgcaga acagtatgat gttcccaagg      600
ggtcaaagaa ccgaaaatgt attcctggtt caatcaagtt ggacagtgaa gaagatatgc      660
catttgaaga ctgcacaaat gatcctgagt cagaacatga cctgttgctt aatggctgtt      720
tgaaatcact ggctttttgat tctgaacatt ctgcagatga gaaggaaaag ccttgtgcta      780
aatctcgagc cagaaagagc tctgataatc caaaaaggac tagtgtgaaa aagggccaca      840
tacaatttga agcacataaa gatgaacgga ggggaaagat tccagagaac cttggcctaa      900
actttatctc tggggatata tctgatacgc aggcctctaa tgaactttcc aggatagcaa      960
atagcctcac agggtccaac actgccccag gaagtttttct gtttttcttcc tgtggaaaaa     1020
acactgcaaa gaaagaattt gagacttcaa atggtgactc tttattgggc ttgcctgagg     1080
gtgctttgat ctcaaagtgt tctcgagaga agaataaacc caacgaagc ctggtgtgtg     1140
gttcaaaagt gaagctctgc tatattggag caggtgatga ggaaaagcga agtgattcca     1200
ttagtatctg taccacttct gatgatggaa gcagtgacct ggatcccata gaacacagct     1260
cagagtctga taacagtgtc cttgaaattc cagatgcttt cgatagaaca gagaacatgt     1320
tatctatgca gaaaaatgaa aagataaagt attctaggtt tgctgccaca aacactaggg     1380
taaaagcaaa acagaagcct ctcattagta actcacatac agaccactta atgggttgta     1440
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ctactcttgt tcacaaaccc cagtcagatt ttacaaatga tgctctctct ccaaaattca     1560
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taaaactact gaacaatatg catgagaaaa ccagggattc aagtgacata gaaacagcag     1860
tggtgaaaca tgtttttatcc gagttgaagg aactctctta cagatcctta ggtgaggatg     1920
tcagtgactc tggaacatca aagccatcaa aaccattact tttctcttct gcttctagtc     1980
agaatcacat acctattgaa ccagactaca aattcagtac attgctaatg atgttgaaag     2040
atatgcatga tagtaagacg aaggagcagc ggttgatgac tgctcaaaac ctggtctctt     2100
accggagtcc tggtcgtggg gactgttcta ctaatagtcc tgtaggagtc tctaaggttt     2160
tggtttcagg aggctccaca cacaattcag agaaaaaggg agatggcact cagaactccg     2220
ccaatcctag ccctagtggg ggtgactctg cattatctgg cgagttgtct gcttccctac     2280
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tgaatcagct tccaagtgtg actcttgatg ctgtactgca gggagaccga aacgtggag     2520
gttcattgag aggtggggca gaagatccta gtaaagagga tcccccttcag ataatgggcc     2580
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aaaaacaaaa gaaggtacag gagcaggtgc acaaggtaag ttcccgctgt gaagaggaaa     3240
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cgccaggaaa ttatgaaagt aaacgtcaaa gaaaaccaac taagaaactt cttgaatcca    3540
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atgaagagtg tgtccagaag tacccaccca ctgttatgca gaacaagggc ttccggtgct    4200
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ctgggaaagc agcagcccct tcagaggacc cctggcaagc tgttaaatca ctcacccagg   6900
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cttatggttg tgtgaaccat gtatgaaaat ccagtgggcc ccaaccaagg agacagacag   7620
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<210> 36
<211> 2696
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

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Ser Asn Pro Val Asn Leu Asp Ala Pro Glu Asp Lys Asp Ser Pro Phe
                20                  25                  30
Gly Asn Gly Gln Ser Asn Phe Ser Glu Pro·Leu Asn Gly Cys Thr Met
            35                  40                  45
Gln Leu Ser Thr Val Ser Gly Thr Ser Gln Asn Ala Tyr Gly Gln Asp
        50                  55                  60
Ser Pro Ser Cys Tyr Ile Pro Leu Arg Arg Leu Gln Asp Leu Ala Ser
65                  70                  75                  80
Met Ile Asn Val Glu Tyr Leu Asn Gly Ser Ala Asp Gly Ser Glu Ser
                85                  90                  95
Phe Gln Asp Pro Glu Lys Ser Asp Ser Arg Ala Gln Thr Pro Ile Val
            100                 105                 110
Cys Thr Ser Leu Ser Pro Gly Gly Pro Thr Ala Leu Ala Met Lys Gln
            115                 120                 125
Glu Pro Ser Cys Asn Asn Ser Pro Glu Leu Gln Val Lys Val Thr Lys
        130                 135                 140
Thr Ile Lys Asn Gly Phe Leu His Phe Glu Asn Phe Thr Cys Val Asp
145                 150                 155                 160
Asp Ala Asp Val Asp Ser Glu Met Asp Pro Glu Gln Pro Val Thr Glu
                165                 170                 175
Asp Glu Ser Ile Glu Glu Ile Phe Glu Glu Thr Gln Thr Asn Ala Thr
            180                 185                 190
Cys Asn Tyr Glu Thr Lys Ser Glu Asn Gly Val Lys Val Ala Met Gly
            195                 200                 205
Ser Glu Gln Asp Ser Thr Pro Glu Ser Arg His Gly Ala Val Lys Ser
        210                 215                 220
Pro Phe Leu Pro Leu Ala Pro Gln Thr Glu Thr Gln Lys Asn Lys Gln
225                 230                 235                 240
Arg Asn Glu Val Asp Gly Ser Asn Glu Lys Ala Ala Leu Leu Pro Ala
                245                 250                 255
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Pro Phe Ser Leu Gly Asp Thr Asn Ile Thr Ile Glu Glu Gln Leu Asn
            260                 265                 270
Ser Ile Asn Leu Ser Phe Gln Asp Asp Pro Asp Ser Ser Thr Ser Thr
            275                 280                 285
Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser Ser Thr Ser
            290                 295                 300
Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr Pro Leu Lys
305                 310                 315                 320
Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg Arg Pro Trp
                325                 330                 335
Trp Pro Cys Arg Ile Cys Ser Asp Pro Leu Ile Asn Thr His Ser Lys
            340                 345                 350
Met Lys Val Ser Asn Arg Arg Pro Tyr Arg Gln Tyr Tyr Val Glu Ala
            355                 360                 365
Phe Gly Asp Pro Ser Glu Arg Ala Trp Val Ala Gly Lys Ala Ile Val
    370                 375                 380
Met Phe Glu Gly Arg His Gln Phe Glu Glu Leu Pro Val Leu Arg Arg
385                 390                 395                 400
Arg Gly Lys Gln Lys Glu Lys Gly Tyr Arg His Lys Val Pro Gln Lys
                405                 410                 415
Ile Leu Ser Lys Trp Glu Ala Ser Val Gly Leu Ala Glu Gln Tyr Asp
            420                 425                 430
Val Pro Lys Gly Ser Lys Asn Arg Lys Cys Ile Pro Gly Ser Ile Lys
            435                 440                 445
Leu Asp Ser Glu Glu Asp Met Pro Phe Glu Asp Cys Thr Asn Asp Pro
    450                 455                 460
Glu Ser Glu His Asp Leu Leu Leu Asn Gly Cys Leu Lys Ser Leu Ala
465                 470                 475                 480
Phe Asp Ser Glu His Ser Ala Asp Glu Lys Glu Lys Pro Cys Ala Lys
                485                 490                 495
Ser Arg Ala Arg Lys Ser Ser Asp Asn Pro Lys Arg Thr Ser Val Lys
            500                 505                 510
Lys Gly His Ile Gln Phe Glu Ala His Lys Asp Glu Arg Arg Gly Lys
            515                 520                 525
Ile Pro Glu Asn Leu Gly Leu Asn Phe Ile Ser Gly Asp Ile Ser Asp
    530                 535                 540
Thr Gln Ala Ser Asn Glu Leu Ser Arg Ile Ala Asn Ser Leu Thr Gly
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Ser Asn Thr Ala Pro Gly Ser Phe Leu Phe Ser Ser Cys Gly Lys Asn
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Thr Ala Lys Lys Glu Phe Glu Thr Ser Asn Gly Asp Ser Leu Leu Gly
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Leu Pro Glu Gly Ala Leu Ile Ser Lys Cys Ser Arg Glu Lys Asn Lys
            595                 600                 605
Pro Gln Arg Ser Leu Val Cys Gly Ser Lys Val Lys Leu Cys Tyr Ile
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Gly Ala Gly Asp Glu Glu Lys Arg Ser Asp Ser Ile Ser Ile Cys Thr
625                 630                 635                 640
Thr Ser Asp Asp Gly Ser Ser Asp Leu Asp Pro Ile Glu His Ser Ser
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Glu Ser Asp Asn Ser Val Leu Glu Ile Pro Asp Ala Phe Asp Arg Thr
            660                 665                 670
Glu Asn Met Leu Ser Met Gln Lys Asn Glu Lys Ile Lys Tyr Ser Arg
            675                 680                 685
Phe Ala Ala Thr Asn Thr Arg Val Lys Ala Lys Gln Lys Pro Leu Ile
    690                 695                 700
Ser Asn Ser His Thr Asp His Leu Met Gly Cys Thr Lys Ser Ala Glu
705                 710                 715                 720
Pro Gly Thr Glu Thr Ser Gln Val Asn Leu Ser Asp Leu Lys Ala Ser
                725                 730                 735
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Pro Lys Phe Asn Leu Ser Ser Ser Ile Ser Ser Glu Asn Ser Leu Ile
        755             760         765
Lys Gly Gly Ala Ala Asn Gln Ala Leu Leu His Ser Lys Ser Lys Gln
    770             775         780
Pro Lys Phe Arg Ser Ile Lys Cys Lys His Lys Glu Asn Pro Val Met
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Ala Glu Pro Pro Val Ile Asn Glu Glu Cys Ser Leu Lys Cys Cys Ser
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Ser Asp Thr Lys Gly Ser Pro Leu Ala Ser Ile Ser Lys Ser Gly Lys
        820         825         830
Val Asp Gly Leu Lys Leu Leu Asn Asn Met His Glu Lys Thr Arg Asp
        835         840         845
Ser Ser Asp Ile Glu Thr Ala Val Val Lys His Val Leu Ser Glu Leu
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Lys Glu Leu Ser Tyr Arg Ser Leu Gly Glu Asp Val Ser Asp Ser Gly
865             870         875             880
Thr Ser Lys Pro Ser Lys Pro Leu Leu Phe Ser Ser Ala Ser Ser Gln
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Asn His Ile Pro Ile Glu Pro Asp Tyr Lys Phe Ser Thr Leu Leu Met
        900         905             910
Met Leu Lys Asp Met His Asp Ser Lys Thr Lys Glu Gln Arg Leu Met
    915         920             925
Thr Ala Gln Asn Leu Val Ser Tyr Arg Ser Pro Gly Arg Gly Asp Cys
    930         935             940
Ser Thr Asn Ser Pro Val Gly Val Ser Lys Val Leu Val Ser Gly Gly
945             950         955             960
Ser Thr His Asn Ser Glu Lys Lys Gly Asp Gly Thr Gln Asn Ser Ala
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Asn Pro Ser Pro Ser Gly Gly Asp Ser Ala Leu Ser Gly Glu Leu Ser
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Ala Ser Leu Pro Gly Leu Leu Ser Asp Lys Arg Asp Leu Pro Ala Ser
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Gly Lys Ser Arg Ser Asp Cys Val Thr Arg Arg Asn Cys Gly Arg Ser
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Lys Pro Ser Ser Lys Leu Arg Asp Ala Phe Ser Ala Gln Met Val Lys
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Asn Thr Val Asn Arg Lys Ala Leu Lys Thr Glu Arg Lys Arg Lys Leu
            1045            1050            1055
Asn Gln Leu Pro Ser Val Thr Leu Asp Ala Val Leu Gln Gly Asp Arg
        1060            1065            1070
Glu Arg Gly Gly Ser Leu Arg Gly Gly Ala Glu Asp Pro Ser Lys Glu
        1075            1080            1085
Asp Pro Leu Gln Ile Met Gly His Leu Thr Ser Glu Asp Gly Asp His
        1090            1095            1100
Phe Ser Asp Val His Phe Asp Ser Lys Val Lys Gln Ser Asp Pro Gly
1105            1110            1115            1120
Lys Ile Ser Glu Lys Gly Leu Ser Phe Glu Asn Gly Lys Gly Pro Glu
            1125            1130            1135
Leu Asp Ser Val Met Asn Ser Glu Asn Asp Glu Leu Asn Gly Val Asn
            1140            1145            1150
Gln Val Val Pro Lys Lys Arg Trp Gln Arg Leu Asn Gln Arg Arg Thr
        1155            1160            1165
Lys Pro Arg Lys Arg Met Asn Arg Phe Lys Glu Lys Glu Asn Ser Glu
    1170            1175            1180
Cys Ala Phe Arg Val Leu Leu Pro Ser Asp Pro Val Gln Glu Gly Arg
1185            1190            1195            1200
Asp Glu Phe Pro Glu His Arg Thr Pro Ser Ala Ser Ile Leu Glu Glu
            1205            1210            1215
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Arg Leu Asn Val Cys Asp Lys Ser Ser Ala Ser Ile Gly Asp Met Glu
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Lys Glu Pro Gly Ile Pro Ser Leu Thr Pro Gln Ala Glu Leu Pro Glu
        1250                1255            1260
Pro Ala Val Arg Ser Glu Lys Lys Arg Leu Arg Lys Pro Ser Lys Trp
1265                1270            1275                1280
Leu Leu Glu Tyr Thr Glu Glu Tyr Asp Gln Ile Phe Ala Pro Lys Lys
        1285                1290            1295
Lys Gln Lys Lys Val Gln Glu Gln Val His Lys Val Ser Ser Arg Cys
        1300                1305            1310
Glu Glu Glu Ser Leu Leu Ala Arg Gly Arg Ser Ser Ala Gln Asn Lys
        1315                1320            1325
Gln Val Asp Glu Asn Ser Leu Ile Ser Thr Lys Glu Glu Pro Pro Val
        1330                1335            1340
Leu Glu Arg Glu Ala Pro Phe Leu Glu Gly Pro Leu Ala Gln Ser Glu
1345                1350            1355                1360
Leu Gly Gly Gly His Ala Glu Leu Pro Gln Leu Thr Leu Ser Val Pro
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Val Ala Pro Glu Val Ser Pro Arg Pro Ala Leu Glu Ser Glu Glu Leu
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Leu Val Lys Thr Pro Gly Asn Tyr Glu Ser Lys Arg Gln Arg Lys Pro
        1395                1400            1405
Thr Lys Lys Leu Leu Glu Ser Asn Asp Leu Asp Pro Gly Phe Met Pro
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Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu Ala Gly His
1425                1430            1435                1440
Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr Ser Lys Asp
        1445                1450            1455
Phe Gly Gly Gly Thr Thr Lys Ile Phe Asp Lys Pro Arg Lys Arg Lys
        1460                1465            1470
Arg Gln Arg His Ala Ala Ala Lys Met Gln Cys Lys Lys Val Lys Asn
        1475                1480            1485
Asp Asp Ser Ser Lys Glu Ile Pro Gly Ser Glu Gly Glu Leu Met Pro
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His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu Gly Val Glu
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His Asp Pro Gly Met Pro Ala Ser Lys Lys Met Gln Gly Glu Arg Gly
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Gly Gly Ala Ala Leu Lys Glu Asn Val Cys Gln Asn Cys Glu Lys Leu
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Gly Glu Leu Leu Leu Cys Glu Ala Gln Cys Cys Gly Ala Phe His Leu
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Glu Cys Leu Gly Leu Thr Glu Met Pro Arg Gly Lys Phe Ile Cys Asn
        1570                1575            1580
Glu Cys Arg Thr Gly Ile His Thr Cys Phe Val Cys Lys Gln Ser Gly
1585                1590            1595                1600
Glu Asp Val Lys Arg Cys Leu Leu Pro Leu Cys Gly Lys Phe Tyr His
        1605                1610            1615
Glu Glu Cys Val Gln Lys Tyr Pro Pro Thr Val Met Gln Asn Lys Gly
        1620                1625            1630
Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala Ala Asn Pro
        1635                1640            1645
Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys Val Arg Cys
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Pro Val Ala Tyr His Ala Asn Asp Phe Cys Leu Ala Ala Gly Ser Lys
1665                1670            1675                1680
Ile Leu Ala Ser Asn Ser Ile Ile Cys Pro Asn His Phe Thr Pro Arg
        1685                1690            1695
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Cys Ser Glu Gly Gly Ser Leu Leu Cys Cys Asp Ser Cys Pro Ala Ala
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Phe His Arg Glu Cys Leu Asn Ile Asp Ile Pro Glu Gly Asn Trp Tyr
    1730                1735                1740
Cys Asn Asp Cys Lys Ala Gly Lys Lys Pro His Tyr Arg Glu Ile Val
1745                1750                1755                1760
Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu Ile Cys His
            1765                1770                1775
Pro Arg Ala Val Pro Ser Asn Ile Asp Lys Met Arg His Asp Val Gly
            1780                1785                1790
Glu Phe Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu Trp Thr His
            1795                1800                1805
Gln Ala Arg Val Phe Pro Tyr Met Glu Gly Asp Val Ser Ser Lys Asp
    1810                1815                1820
Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala Leu Gln Glu
1825                1830                1835                1840
Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu Leu Arg Gln
            1845                1850                1855
Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro Tyr Lys His
            1860                1865                1870
Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe Thr Ala Asp
            1875                1880                1885
Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp Glu Asn Pro
    1890                1895                1900
Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu Tyr Glu Cys
1905                1910                1915                1920
His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn Gln Cys Phe
            1925                1930                1935
Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr Leu Gln Arg
            1940                1945                1950
Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly Glu Phe Val
    1955                1960                1965
Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys Arg Ala Arg
    1970                1975                1980
Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr Met Leu Thr
1985                1990                1995                2000
Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly Asn Tyr Ala
            2005                2010                2015
Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr Gln Lys Trp
            2020                2025                2030
Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu Ser Asp Ile
            2035                2040                2045
Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu Cys Leu Gly
    2050                2055                2060
Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys Ser Gly Phe
2065                2070                2075                2080
Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu Glu Lys Ser
            2085                2090                2095
Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr Gln Gly Glu
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Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly Asp Ala Gly
            2115                2120                2125
Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val Tyr His Ala
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Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp Glu Cys Pro
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Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser Phe Cys Glu
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54

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     2210                2215                2220
Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala Glu Gln Ser
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Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys Pro Pro Ala
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Asp Thr Asn Gln Met Leu Ser Leu Ser Lys Lys Ala Leu Ala Gly Thr
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Cys Gln Arg Pro Leu Leu Pro Glu Arg Pro Leu Glu Arg Thr Asp Ser
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Arg Pro Gln Pro Leu Asp Lys Val Arg Asp Leu Ala Gly Ser Gly Thr
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Ser Pro Arg Pro Gln Ser Leu Glu Lys Thr Ser Val Pro Thr Gly Leu
     2370                2375                2380
Arg Leu Pro Pro Pro Asp Arg Leu Leu Ile Thr Ser Ser Pro Lys Pro
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Arg Leu Pro Pro Pro Glu Lys Val Leu Ser Ala Val Val Gln Thr Leu
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Val Ala Lys Glu Lys Ala Leu Arg Pro Val Asp Gln Asn Thr Gln Ser
          2435                2440                2445
Lys Asn Arg Ala Ala Leu Val Met Asp Leu Ile Asp Leu Thr Pro Arg
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Gln Lys Glu Arg Ala Ala Ser Pro His Gln Val Thr Pro Gln Ala Asp
2465                2470                2475                2480
Glu Lys Met Pro Val Leu Glu Ser Ser Ser Trp Pro Ala Ser Lys Gly
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Leu Gly His Met Pro Arg Ala Val Glu Lys Gly Cys Val Ser Asp Pro
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Leu Gln Thr Ser Gly Lys Ala Ala Ala Pro Ser Glu Asp Pro Trp Gln
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Ala Val Lys Ser Leu Thr Gln Ala Arg Leu Leu Ser Gln Pro Pro Ala
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Lys Ala Phe Leu Tyr Glu Pro Thr Thr Gln Ala Ser Gly Arg Ala Ser
2545                2550                2555                2560
Ala Gly Ala Glu Gln Thr Pro Gly Pro Leu Ser Gln Ser Pro Gly Leu
          2565                2570                2575
Val Lys Gln Ala Lys Gln Met Val Gly Gly Gln Gln Leu Pro Ala Leu
          2580                2585                2590
Ala Ala Lys Ser Gly Gln Ser Phe Arg Ser Leu Gly Lys Ala Pro Ala
          2595                2600                2605
Ser Leu Pro Thr Glu Glu Lys Lys Leu Val Thr Thr Glu Gln Ser Pro
     2610                2615                2620
Trp Ala Leu Gly Lys Ala Ser Ser Arg Ala Gly Leu Trp Pro Ile Val
2625                2630                2635                2640
Ala Gly Gln Thr Leu Ala Gln Ser Cys Trp Ser Ala Gly Ser Thr Gln
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Thr Leu Ala Gln Thr Cys Trp Ser Leu Gly Arg Gly Gln Asp Pro Lys
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Pro Glu Gln Asn Thr Leu Pro Ala Leu Asn Gln Ala Pro Ser Ser His
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Lys Cys Ala Glu Ser Glu Gln Lys
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```

<210> 38
<211> 1784
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 38

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Asp Thr Gln Pro Ile Leu Leu Gln Ser Cys Thr Gly Leu Val Thr His
            20                  25                  30
Arg Leu Leu Glu Glu Asp Thr Pro Arg Tyr Met Arg Ala Ser Asp Pro
         35                  40                  45
Ala Ser Pro His Ile Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp
     50                  55                  60
Ser Ser Leu Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser
 65                  70                  75                  80
```

58

```
Gly Val His Gly Asp Ser Pro Tyr Gly Ser Gly Thr Met Asp Thr His
                85              90              95
Ser Leu Glu Ser Lys Ala Glu Arg Ile Ala Arg Tyr Lys Ala Glu Arg
            100             105             110
Arg Arg Gln Leu Ala Glu Lys Tyr Gly Leu Thr Leu Asp Pro Glu Ala
            115             120             125
Asp Ser Glu Tyr Leu Ser Arg Tyr Thr Lys Ser Arg Lys Glu Pro Asp
        130             135             140
Ala Val Glu Lys Arg Gly Gly Lys Ser Asp Lys Gln Glu Glu Ser Ser
    145             150             155             160
Arg Asp Ala Ser Ser Leu Tyr Pro Gly Thr Glu Thr Met Gly Leu Arg
            165             170             175
Thr Cys Ala Gly Glu Ser Lys Asp Tyr Ala Leu His Ala Gly Asp Gly
            180             185             190
Ser Ser Asp Pro Glu Val Leu Leu Asn Ile Glu Asn Gln Arg Arg Gly
            195             200             205
Gln Glu Leu Ser Ala Thr Arg Gln Ala His Asp Leu Ser Pro Ala Ala
    210             215             220
Glu Ser Ser Ser Thr Phe Ser Phe Ser Gly Arg Asp Ser Ser Phe Thr
225             230             235             240
Glu Val Pro Arg Ser Pro Lys His Ala His Ser Ser Ser Leu Gln Gln
            245             250             255
Ala Ala Ser Arg Ser Pro Ser Phe Gly Asp Pro Gln Leu Ser Pro Glu
            260             265             270
Ala Arg Pro Arg Cys Thr Ser His Ser Glu Thr Pro Thr Val Asp Asp
            275             280             285
Glu Glu Lys Val Asp Glu Arg Ala Lys Leu Ser Val Ala Ala Lys Arg
    290             295             300
Leu Leu Phe Arg Glu Met Glu Lys Ser Phe Asp Glu Gln Asn Val Pro
305             310             315             320
Lys Arg Arg Ser Arg Asn Thr Ala Val Glu Gln Arg Leu Arg Arg Leu
            325             330             335
Gln Asp Arg Ser Leu Thr Gln Pro Ile Thr Thr Glu Glu Val Val Ile
            340             345             350
Ala Ala Thr Leu Gln Ala Ser Ala His Gln Lys Ala Leu Ala Lys Asp
            355             360             365
Gln Thr Asn Glu Gly Lys Glu Leu Ala Glu Gln Gly Glu Pro Asp Ser
    370             375             380
Ser Thr Leu Ser Leu Ala Glu Lys Leu Ala Leu Phe Asn Lys Leu Ser
385             390             395             400
Gln Pro Val Ser Lys Ala Ile Ser Thr Arg Asn Arg Ile Asp Thr Arg
            405             410             415
Gln Arg Arg Met Asn Ala Arg Tyr Gln Thr Gln Pro Val Thr Leu Gly
            420             425             430
Glu Val Glu Gln Val Gln Ser Gly Lys Leu Ile Pro Phe Ser Pro Ala
            435             440             445
Val Asn Thr Ser Val Ser Thr Val Ala Ser Thr Val Ala Pro Met Tyr
    450             455             460
Ala Gly Asp Leu Arg Thr Lys Pro Pro Leu Asp His Asn Ala Ser Ala
465             470             475             480
Thr Asp Tyr Lys Phe Ser Ser Ser Ile Glu Asn Ser Asp Ser Pro Val
            485             490             495
Arg Ser Ile Leu Lys Ser Gln Ala Trp Gln Pro Leu Val Glu Gly Ser
            500             505             510
Glu Asn Lys Gly Met Leu Arg Glu Tyr Gly Glu Thr Glu Ser Lys Arg
            515             520             525
Ala Leu Thr Gly Arg Asp Ser Gly Met Glu Lys Tyr Gly Ser Phe Glu
    530             535             540
Glu Ala Glu Ala Ser Tyr Pro Ile Leu Asn Arg Ala Arg Glu Gly Asp
545             550             555             560
```

59

```
Ser His Lys Glu Ser Lys Tyr Ala Val Pro Arg Arg Gly Ser Leu Glu
            565             570             575
Arg Ala Asn Pro Pro Ile Thr His Leu Gly Asp Glu Pro Lys Glu Phe
            580             585             590
Ser Met Ala Lys Met Asn Ala Gln Gly Asn Leu Asp Leu Arg Asp Arg
            595             600             605
Leu Pro Phe Glu Glu Lys Val Glu Val Glu Asn Val Met Lys Arg Lys
    610             615             620
Phe Ser Leu Arg Ala Ala Glu Phe Gly Glu Pro Thr Ser Glu Gln Thr
625             630             635             640
Gly Thr Ala Ala Gly Lys Thr Ile Ala Gln Thr Thr Ala Pro Val Ser
            645             650             655
Trp Lys Pro Gln Asp Ser Ser Glu Gln Pro Gln Glu Lys Leu Cys Lys
            660             665             670
Asn Pro Cys Ala Met Phe Ala Ala Gly Glu Ile Lys Thr Pro Thr Gly
            675             680             685
Glu Gly Leu Leu Asp Ser Pro Ser Lys Thr Met Ser Ile Lys Glu Arg
    690             695             700
Leu Ala Leu Leu Lys Lys Ser Gly Glu Glu Asp Trp Arg Asn Arg Leu
705             710             715             720
Ser Arg Arg Gln Glu Gly Gly Lys Ala Pro Ala Ser Ser Leu His Thr
            725             730             735
Gln Glu Ala Gly Arg Ser Leu Ile Lys Lys Arg Val Thr Glu Ser Arg
            740             745             750

Glu Ser Gln Met Thr Ile Glu Glu Arg Lys Gln Leu Ile Thr Val Arg
            755             760             765
Glu Glu Ala Trp Lys Thr Arg Gly Arg Gly Ala Ala Asn Asp Ser Thr
    770             775             780
Gln Phe Thr Val Ala Gly Arg Met Val Lys Lys Gly Leu Ala Ser Pro
785             790             795             800
Thr Ala Ile Thr Pro Val Ala Ser Ala Ile Cys Gly Lys Thr Arg Gly
            805             810             815
Thr Thr Pro Val Ser Lys Pro Leu Glu Asp Ile Glu Ala Arg Pro Asp
            820             825             830
Met Gln Leu Glu Ser Asp Leu Lys Leu Asp Arg Leu Glu Thr Phe Leu
            835             840             845
Arg Arg Leu Asn Asn Lys Val Gly Gly Met His Glu Thr Val Leu Thr
    850             855             860
Val Thr Gly Lys Ser Val Lys Glu Val Met Lys Pro Asp Asp Asp Glu
865             870             875             880
Thr Phe Ala Lys Phe Tyr Arg Ser Val Asp Tyr Asn Met Pro Arg Ser
            885             890             895
Pro Val Glu Met Asp Glu Asp Phe Asp Val Ile Phe Asp Pro Tyr Ala
            900             905             910
Pro Lys Leu Thr Ser Ser Val Ala Glu His Lys Arg Ala Val Arg Pro
            915             920             925
Lys Arg Arg Val Gln Ala Ser Lys Asn Pro Leu Lys Met Leu Ala Ala
    930             935             940
Arg Glu Asp Leu Leu Gln Glu Tyr Thr Glu Gln Arg Leu Asn Val Ala
945             950             955             960
Phe Met Glu Ser Lys Arg Met Lys Val Glu Lys Met Ser Ser Asn Ser
            965             970             975
Asn Phe Ser Glu Val Thr Leu Ala Gly Leu Ala Ser Lys Glu Asn Phe
            980             985             990
Ser Asn Val Ser Leu Arg Ser Val Asn Leu Thr Glu Gln Asn Ser Asn
            995             1000            1005
Asn Ser Ala Val Pro Tyr Lys Arg Leu Met Leu Leu Gln Ile Lys Gly
    1010            1015            1020
Arg Arg His Val Gln Thr Arg Leu Val Glu Pro Arg Ala Ser Ala Leu
1025            1030            1035            1040
```

60

```
Asn Ser Gly Asp Cys Phe Leu Leu Leu Ser Pro His Cys Cys Phe Leu
            1045                1050                1055
Trp Val Gly Glu Phe Ala Asn Val Ile Glu Lys Ala Lys Ala Ser Glu
            1060                1065                1070
Leu Ala Thr Leu Ile Gln Thr Lys Arg Glu Leu Gly Cys Arg Ala Thr
            1075                1080                1085
Tyr Ile Gln Thr Ile Glu Glu Gly Ile Asn Thr His Thr His Ala Ala
            1090                1095                1100
Lys Asp Phe Trp Lys Leu Leu Gly Gly Gln Thr Ser Tyr Gln Ser Ala
1105                1110                1115                1120
Gly Asp Pro Lys Glu Asp Glu Leu Tyr Glu Ala Ala Ile Ile Glu Thr
            1125                1130                1135
Asn Cys Ile Tyr Arg Leu Met Asp Asp Lys Leu Val Pro Asp Asp Asp
            1140                1145                1150
Tyr Trp Gly Lys Ile Pro Lys Cys Ser Leu Leu Gln Pro Lys Glu Val
            1155                1160                1165
Leu Val Phe Asp Phe Gly Ser Glu Val Tyr Val Trp His Gly Lys Glu
            1170                1175                1180
Val Thr Leu Ala Gln Arg Lys Ile Ala Phe Gln Leu Ala Lys His Leu
1185                1190                1195               1200
Trp Asn Gly Thr Phe Asp Tyr Glu Asn Cys Asp Ile Asn Pro Leu Asp
             1205                1210                1215
Pro Gly Glu Cys Asn Pro Leu Ile Pro Arg Lys Gly Gln Gly Arg Pro
            1220                1225                1230
Asp Trp Ala Ile Phe Gly Arg Leu Thr Glu His Asn Glu Thr Ile Leu
            1235                1240                1245
Phe Lys Glu Lys Phe Leu Asp Trp Thr Glu Leu Lys Arg Ser Asn Glu
            1250                1255                1260
Lys Asn Pro Gly Glu Leu Ala Gln His Lys Glu Asp Pro Arg Thr Asp
1265                1270                1275                1280
Val Lys Ala Tyr Asp Val Thr Arg Met Val Ser Met Pro Gln Thr Thr
            1285                1290                1295
Ala Gly Thr Ile Leu Asp Gly Val Asn Val Gly Arg Gly Tyr Gly Leu
            1300                1305                1310
Val Glu Gly His Asp Arg Arg Gln Phe Glu Ile Thr Ser Val Ser Val
            1315                1320                1325
Asp Val Trp His Ile Leu Glu Phe Asp Tyr Ser Arg Leu Pro Lys Gln
            1330                1335                1340
Ser Ile Gly Gln Phe His Glu Gly Asp Ala Tyr Val Val Lys Trp Lys
1345                1350                1355                1360
Phe Met Val Ser Thr Ala Val Gly Ser Arg Gln Lys Gly Glu His Ser
            1365                1370                1375
Val Arg Ala Ala Gly Lys Glu Lys Cys Val Tyr Phe Phe Trp Gln Gly
            1380                1385                1390
Arg His Ser Thr Val Ser Glu Lys Gly Thr Ser Ala Leu Met Thr Val
            1395                1400                1405
Glu Leu Asp Glu Glu Arg Gly Ala Gln Val Gln Val Leu Gln Gly Lys
            1410                1415                1420
Glu Pro Pro Cys Phe Leu Gln Cys Phe Gln Gly Gly Met Val Val His
1425                1430                1435                1440
Ser Gly Arg Arg Glu Glu Glu Glu Glu Asn Val Gln Ser Glu Trp Arg
            1445                1450                1455
Leu Tyr Cys Val Arg Gly Glu Val Pro Val Glu Gly Asn Leu Leu Glu
            1460                1465                1470
Val Ala Cys His Cys Ser Ser Leu Arg Ser Arg Thr Ser Met Val Val
            1475                1480                1485
Leu Asn Val Asn Lys Ala Leu Ile Tyr Leu Trp His Gly Cys Lys Ala
            1490                1495                1500
Gln Ala His Thr Lys Glu Val Gly Arg Thr Ala Ala Asn Lys Ile Lys
1505                1510                1515                1520
```

```
Glu Gln Cys Pro Leu Glu Ala Gly Leu His Ser Ser Ser Lys Val Thr
            1525                1530                1535
Ile His Glu Cys Asp Glu Gly Ser Glu Pro Leu Gly Phe Trp Asp Ala
            1540                1545                1550
Leu Gly Arg Arg Asp Arg Lys Ala Tyr Asp Cys Met Leu Gln Asp Pro
        1555                1560                1565
Gly Ser Phe Asn Phe Ala Pro Arg Leu Phe Ile Leu Ser Ser Ser Ser
    1570                1575                1580
Gly Asp Phe Ala Ala Thr Glu Phe Val Tyr Pro Ala Arg Ala Pro Ser
1585                1590                1595                1600
Val Val Ser Ser Met Pro Phe Leu Gln Glu Asp Leu Tyr Ser Ala Pro
            1605                1610                1615
Gln Pro Ala Leu Phe Leu Val Asp Asn His His Glu Val Tyr Leu Trp
            1620                1625                1630
Gln Gly Trp Trp Pro Ile Glu Asn Lys Ile Thr Gly Ser Ala Arg Ile
            1635                1640                1645
Arg Trp Ala Ser Asp Arg Lys Ser Ala Met Glu Thr Val Leu Gln Tyr
    1650                1655                1660
Cys Lys Gly Lys Asn Leu Lys Lys Pro Ala Pro Lys Ser Tyr Leu Ile
1665                1670                1675                1680
His Ala Gly Leu Glu Pro Leu Thr Phe Thr Asn Met Phe Pro Ser Trp
            1685                1690                1695
Glu His Arg Glu Asp Ile Ala Glu Ile Thr Glu Met Asp Thr Glu Val
            1700                1705                1710
Ser Asn Gln Ile Thr Leu Val Glu Asp Val Leu Ala Lys Leu Cys Lys
        1715                1720                1725
Thr Ile Tyr Pro Leu Ala Asp Leu Leu Ala Arg Pro Leu Pro Glu Gly
    1730                1735                1740
Val Asp Pro Leu Lys Leu Glu Ile Tyr Leu Thr Asp Glu Asp Phe Glu
1745                1750                1755                1760
Phe Ala Leu Asp Met Thr Arg Asp Glu Tyr Asn Ala Leu Pro Ala Trp
            1765                1770                1775
Lys Gln Val Asn Leu Lys Lys Ala
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```

<210> 39
<211> 6719
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 39
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ctcactgagt tttgactagc ggaagaaaag agagagttca agtggatggc cttgaggact     180
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cggcgttaag atttcaacaa gaaaaactta agcttccttg gattcccacg tcaaaggaaa     300
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tttgaaccaa agaagaaaga attcttagaa atgaaaagaa aagaaagaat tgccaggcgc     480
ctggaaggga ttgaaaatga cactcagccc atcctcttgc agagctgcac aggattggtg     540
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ggtaccatgg acacccacag tctggagtcc aaagccgaaa gaattgcaag gtacaaagca     780
gaaagaaggc gacagctggc agagaagtat gggctgactc tggatcccga ggccgactcc     840
gagtatttat cccgctatac caagtccagg aaggagcctg atgctgtcga gaagcgggga     900
ggaaaaagtg acaaacagga gagtcaagc agagatgcga gttctctgta ccccgggacc     960
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gagacgatgg ggctcaggac ctgtgccggt gaatccaagg actatgccct ccatgcgggt   1020
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ctgagtgcca cccggcaggc ccatgacctg tccccagcag ccgagagttc ctcgaccttc   1140
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63

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cagtgtttcc aggggggggat ggtggtgcac tcggggaggc gggaagagga agaagaaaat    4800
gtgcaaagtg agtggcggct gtactgcgtg cgtggagagg tgcccgtgga agggaatttg    4860
ctggaagtgg cctgtcactg tagcagcctg aggtccagaa cttccatggt ggtgcttaac    4920
gtcaacaagg ccctcatcta cctgtggcac ggatgcaaag cccaggccca cacgaaggag    4980
gtcggaagga ccgctgcgaa caagatcaag gaacaatgtc ccctggaagc aggactgcat    5040
agtagcagca aagtcacaat acacgagtgt gatgaaggct ccgagccact cggattctgg    5100
gatgccttag gaaggagaga caggaaagcc tacgattgca tgcttcaaga tcctggaagt    5160
tttaacttcg cgccccgcct gttcatcctc agcagctcct ctggggattt tgcagccaca    5220
gagtttgtgt accctgcccg agccccctct gtggtcagtt ccatgccctt cctgcaggaa    5280
gatctgtaca gcgcgcccca gccagcactt ttccttgttg acaatcacca cgaggtgtac    5340
ctctggcaag gctggtggcc catcgagaac aagatcactg gttccgcccg catccgctgg    5400
gcctccgacc ggaagagtgc gatggagact gtgctccagt actgcaaagg aaaaaatctc    5460
aagaaaccag ccccccaagtc ttaccttatc cacgctggtc tggagccccct gacattcacc    5520
aatatgtttc ccagctggga gcacagagag gacatcgctg agatcacaga gatggacacg    5580
gaagtttcca atcagatcac cctcgtggaa gacgtcttag ccaagctctg taaaaccatt    5640
tacccgctgg ccgacctcct ggccaggcca ctcccggagg gggtcgatcc tctgaagctt    5700
gagatctatc tcaccgacga agacttcgag tttgcactag acatgacgag ggatgaatac    5760
aacgccctgc ccgcctggaa gcaggtgaac ctgaagaaag caaaaggcct gttctgagtg    5820
gggagacgcc agaggagcct cacggtcacg tccaacaaca ccactgcacc agggaaatgg    5880
atatatattt ttggactggt gttttttcaca aagtattttt caatcagagt tttcagaacc    5940
tgacattgtt aaagatactg cttgtcccgg agttgtgtat tttgtaaatg ttcaagggaa    6000
ctgtttggaa acttctttcc accattcagg aggttatcag aattaataaa agtatctgtt    6060
atgtgcactt aagccgcagc tgctatagat agcactgcct tcttgttcca gctaggcaat    6120
gccttttttt ttttttttga agcagttctc tttataaagt gttattttga tagtttgtgg    6180
attctaaaat atatatatat ttatataaac accatataag tcaaatatgt atttaacaaa    6240
gcaatatgta ttcattcact ttcaagattt gttttggtgt caaaataaca tgaaaaggta    6300
gatggagttg cttctgttga attagctctg ccaccaatat gtatcttcat acacgtttgg    6360
aaatgtttcc tgcagcatta ggtatgactt gttctgagta ctgcttccgg tgctaaaatg    6420
aacaaagaat ttgtacttaa tggcatggac tctggagaat ctatgcgaat caacctttct    6480
accttaatat ctccccaaaa atgtatagtg ccttgttttt atgtacagtt tatatacaga    6540
aaagtttgct ctgcattttt gatgatggtt tggaacatta tctacaattt tactctcaaa    6600
tagtcaaaat aaaaacatct caatttctaa taccggttgt aaacaaacag tacacatgtc    6660
attttgtgat ataggactcc caaataaaag tatcagaata aacacaacaa ttaactggt     6719
```

<210> 40
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
       synthetic construct

<400> 40

```
Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys Glu Pro Gly
 1               5                  10                  15
Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro Val Pro Pro
            20                  25                  30
Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val Ile Leu Lys
        35                  40                  45
Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu His Tyr Trp
    50                  55                  60
Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala Ala Ile Phe
65                  70                  75                  80
Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val Gln His Arg
                85                  90                  95
```

```
Glu Val Gln Gly Phe Glu Ser Ser Thr Phe Ser Gly Tyr Phe Lys Ser
            100                     105             110
Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe Lys His Val
            115                 120             125
Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val Lys Gly Arg
    130                     135             140
Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Asp Ser Phe Asn
145                 150                     155                 160
Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile Tyr Gln Trp
                165                 170                     175
Cys Gly Ser Gly Ser Asn Lys Phe Glu Arg Leu Lys Ala Thr Gln Val
            180                     185             190
Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala Gln Val His
        195                 200                 205
Val Ser Glu Glu Glu Thr Glu Pro Glu Ala Met Leu Gln Val Leu Gly
    210                     215             220
Pro Lys Pro Ala Leu Pro Glu Gly Thr Glu Asp Thr Ala Lys Glu Asp
225                     230             235                 240
Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser Asn Gly Ala
                245                 250                 255
Gly Ser Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro Phe Ala Gln
            260                 265                 270
Gly Pro Leu Arg Ser Glu Asp Cys Phe Ile Leu Asp His Gly Arg Asp
            275                 280                 285
Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Met Glu Glu Arg
    290                 295                 300
Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Ser Lys Met Gln Tyr
305                 310                 315                 320
Pro Arg Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly Glu Thr Pro
            325                 330                 335
Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp Gln Thr Asp
            340                 345                 350
Gly Pro Gly Leu Gly Tyr Leu Ser Ser His Ile Ala Asn Val Glu Arg
        355                 360                 365
Val Pro Phe Asp Ala Gly Thr Leu His Thr Ser Thr Ala Met Ala Ala
    370                 375                 380
Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln Ile Trp Arg
385                 390                 395                 400
Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr Tyr Gly Gln
            405                 410                 415
Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr Arg His Gly
            420                 425                 430
Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala Gln Ser Thr
            435                 440                 445
Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln Leu Asp Glu
    450                 455                 460
Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln Gly Lys Glu
465                 470                 475                 480
Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met Ile Ile Tyr
                485                 490                 495
Lys Gly Gly Thr Ser Arg Asp Gly Gly Gln Thr Ala Pro Ala Ser Ile
            500                 505                 510
Arg Leu Phe Gln Val Arg Ala Ser Ser Ser Gly Ala Thr Arg Ala Val
            515                 520                 525
Glu Val Met Pro Lys Ser Gly Ala Leu Asn Ser Asn Asp Ala Phe Val
    530                 535                 540
Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Ala Gly Ala Ser
545                 550                 555                 560
Glu Ala Glu Lys Thr Ala Ala Gln Glu Leu Leu Lys Val Leu Arg Ser
                565                 570                 575
```

65

```
Gln His Val Gln Val Glu Glu Gly Ser Glu Pro Asp Gly Phe Trp Glu
            580                 585             590
Ala Leu Gly Gly Lys Thr Ser Tyr Arg Thr Ser Pro Arg Leu Lys Asp
            595                 600             605
Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys Ser Asn Arg
        610             615             620
Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu Met Gln Glu
625                 630             635                 640
Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp Asp Gln Val
            645                 650             655
Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys Thr Glu Ala
            660                 665             670
Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala Asn Arg Asp
            675                 680             685
Arg Arg Thr Pro Ile Thr Val Val Arg Gln Gly Phe Glu Pro Pro Ser
        690                 695             700
Phe Val Gly Trp Phe Leu Gly Trp Asp Asn Asn Tyr Trp Ser Val Asp
705                 710                 715                 720
Pro Leu Asp Arg Ala Leu Ala Glu Leu Ala Ala
            725                 730
```

<210> 41
<211> 2447
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 41
```
tgagcgcggc ccagcactat ggtggtggag caccccgaat tcctgaaggc agggaaggag      60
cctggcctgc agatctggcg tgtggagaag tttgacctgg tgcctgtgcc ccccaacctc     120
tatggagact tcttcacggg tgatgcctat gtcatcctga agactgtgca gctgaggaat     180
gggaatctgc agtatgacct ccactattgg ctgggcaatg aatgcagcca ggatgagagc     240
ggggctgctg ccatctttac tgtgcaactg gatgactacc tgaacggccg ggctgtgcag     300
caccgtgagg ttcagggctt tgagtcgtcc accttctccg gctacttcaa gtctggactt     360
aagtacaaga aggaggtgt ggcatctgga ttcaaacacg tggtacccaa tgaggtggtg     420
gtccagaggc tcttccaggt caaaggacgc cgtgtagtcc gtgctactga ggtacctgtg     480
tcctgggaca gtttcaacaa tggcgactgc ttcattctgg acctgggaaa caatatctat     540
cagtggtgtg gctctggcag caacaaattt gaaaggctga aggccacaca ggtgtccaag     600
ggcatccggg acaacgagag gagtggccgt gctcaagtac acgtgtctga gaggagact     660
gagcccgagg cgatgctgca ggtgctgggc cccaagccgg ctctgcctga aggtaccgag     720
gacacagcca aggaagatgc agccaaccgc aagctggcca agctctacaa ggtctccaac     780
ggtgcaggta gcatgtcagt ctccctagtg gctgatgaga accccttcgc ccagggggcc     840
ctgagatctg aggactgctt catcctggac catggcagag atgggaaaat ctttgtttgg     900
aaaggcaagc aggccaacat ggaggagcgg aaggctgccc tcaaaacagc ctctgacttc     960
atctccaaga tgcagtaccc caggcagacc caggtttcag ttctcccaga gggcggtgag    1020
accectctct ttaagcagtt cttcaagaac tggcgggacc cagaccagac agatggcccc    1080
ggcctgggct acctctccag ccacattgcc aacgtggagc gcgtaccttt cgatgccggc    1140
acgctgcaca cctccaccgc catggccgct cagcacggca tggatgatga tggaactggc    1200
cagaaacaga tctggagaat tgaaggttcc aacaaggtgc cagtggaccc tgccacatac    1260
ggacagttct atggaggcga cagctacatc attctgtaca actaccgcca cggtggccgc    1320
cagggacaga tcatctacaa ctggcagggt gctcagtcta cccaggatga ggttgctgct    1380
tctgccatcc tgactgccca gctggatgag gagctgggag gaactcctgt ccagagccga    1440
gtggtccaag gcaaagagcc tgcacacctc atgagcttgt ttggcgggaa gcccatgatc    1500
atctacaagg gtggcacctc ccgtgatggt gggcagacag ctcctgccag tatccgcctc    1560
ttccaagtgc gtgccagcag ctctggagcc accagggctg tggaggtgat gcctaagtct    1620
ggtgctctga actccaacga tgcctttgtg ctgaaaaccc cctccgctgc ctacctgtgg    1680
gtgggcgcag agccagtga ggcagagaag acggcggccc aggagcttct gaaggtcctt    1740
cggtcccagc atgtgcaggt ggaagaaggc agtgagccag atggcttctg ggaggctctg    1800
```

```
ggcgggaaga cgtcctaccg cacatccccc aggcttaagg acaagaagat ggatgcccat      1860
cctcctcgac tctttgcctg ctccaacagg atcggacgct ttgtgatcga agaggttcct      1920
ggcgagctta tgcaggaaga cctggctact gatgacgtca tgctcctgga cacctgggac      1980
caggtctttg tctgggttgg aaaagactcc caggaagaag aaaagacgga agccttgact      2040
tctgctaagc ggtacatcga gacagatcca gcaaatcggg acaggcggac ccccatcaca      2100
gtcgttaggc agggctttga gcctccttcc ttcgtgggct ggttcctcgg ctgggacaac      2160
aactactggt cggtggatcc tttggaccgg gccttggctg agctggctgc ctgagtaagg      2220
accaagccat caatgtcacc aatcagtgcc tttgagggtt gtccatctcc caaagacatc      2280
atatggcaag caggaaaact atgatgtgtg cgcgcgtgtt tttgtttttg ttttttacgg      2340
tagccaaaac aagcccttgt ggaaactcag ggtctttaca gaattgcttc aaatgtctgt      2400
actttggaaa tgaaagccaa taaaagcttt ttgaagtgaa aaaaaaa                    2447
```

<210> 42
<211> 928
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 42
```
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
 1               5                  10                  15
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp
            20              25              30
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
            35              40              45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
    50              55              60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65              70              75                  80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
                85              90              95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
            100             105             110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
            115             120             125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
    130             135             140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145             150             155             160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
            165             170             175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
            180             185             190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
            195             200             205
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
    210             215             220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225             230             235             240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
            245             250             255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
            260             265             270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
            275             280             285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
    290             295             300
```

67

```
Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305                 310             315                 320
Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
            325             330                 335
Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
            340             345                 350
Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
            355             360                 365
Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
    370                 375             380
Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385             390                 395                 400
Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
            405             410                 415
Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
            420             425                 430
Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
            435             440                 445
Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
    450             455                 460
Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465                 470             475                 480
Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
            485             490                 495
Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
            500             505                 510
Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
            515             520                 525
Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
    530             535                 540
Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545                 550             555                 560
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
            565             570                 575
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
            580             585                 590
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
            595             600                 605
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
    610             615                 620
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625                 630                 635                 640
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
            645             650                 655
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
            660             665                 670
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
            675             680                 685
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690             695                 700
Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705             710                 715                 720
Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
            725             730                 735
Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
            740             745                 750
Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
            755             760                 765
Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770             775                 780
```

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```
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785                 790             795                 800
Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
                805             810                 815
Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820             825             830
Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
        835             840             845
Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850             855             860
Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865             870             875                 880
Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
            885             890             895
Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
            900             905             910
Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
        915             920             925
```

<210> 43
<211> 2994
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 43

```
ttccggtttt tctcagggga cgttgaaatt atttttgtaa cgggagtcgg gagaggacgg     60
ggcgtgcccc gcgtgcgcgc gcgtcgtcct ccccggcgct cctccacagc tcgctggctc    120
ccgccgcgga aaggcgtcat gccgcccaaa acccccgaa aaacggccgc caccgccgcc     180
gctgccgccg cggaaccccc ggcaccgccg ccgccgcccc ctcctgagga ggacccagag    240
caggacagcg gcccggagga cctgcctctc gtcaggcttg agtttgaaga aacagaagaa    300
cctgatttta ctgcattatg tcagaaatta aagataccag atcatgtcag agagagagct    360
tggttaactt gggagaaagt ttcatctgtg gatggagtat gggaggtta tattcaaaag     420
aaaaaggaac tgtggggaat ctgtatcttt attgcagcag ttgacctaga tgagatgtcg    480
ttcactttta ctgagctaca gaaaaacata gaaatcagtg tccataaatt ctttaactta    540
ctaaaagaaa ttgataccag taccaaagtt gataatgcta tgtcaagact gttgaagaag    600
tatgatgtat tgtttgcact cttcagcaaa ttggaaagga catgtgaact tatatatttg    660
acacaacccca gcagttcgat atctactgaa ataaattctg cattggtgct aaaagtttct    720
tggatcacat ttttattagc taaaggggaa gtattacaaa tggaagatga tctggtgatt    780
tcatttcagt taatgctatg tgtccttgac tatttttatta aactctcacc tcccatgttg    840
ctcaaagaac catataaaac agctgttata cccattaatg gttcacctcg aacacccagg    900
cgaggtcaga acaggagtgc acggatagca aaacaactag aaaatgatac aagaattatt    960
gaagttctct gtaaagaaca tgaatgtaat atagatgagg tgaaaaatgt ttatttcaaa   1020
aattttatac cttttatgaa ttctcttgga cttgtaacat ctaatggact tccagaggtt   1080
gaaaatcttt ctaaacgata cgaagaaatt tatcttaaaa ataaagatct agatgcaaga   1140
ttatttttgg atcatgataa aactcttcag actgattcta tagacagttt tgaaacacag   1200
agaacaccac gaaaaagtaa ccttgatgaa gaggtgaatg taattcctcc acacactcca   1260
gttaggactg ttatgaacac tatccaacaa ttaatgatga ttttaaattc agcaagtgat   1320
caaccttcag aaaatctgat ttcctatttt aacaactgca cagtgaatcc aaaagaaagt   1380
atactgaaaa gagtgaagga tataggatac atctttaaag agaaatttgc taaagctgtg   1440
ggacagggtt gtgtcgaaat tggatcacag cgatacaaac ttggagttcg cttgtattac   1500
cgagtaatgg aatccatgct taaatcagaa gaagaacgat tatccattca aaatttttagc   1560
aaacttctga atgacaacat ttttcatatg tctttattgg cgtgcgctct tgaggttgta   1620
atggccacat atagcagaag tacatctcag aatcttgatt ctggaacaga tttgtctttc   1680
ccatggattc tgaatgtgct taatttaaaa gcctttgatt tttacaaagt gatcgaaagt   1740
tttatcaaag cagaaggcaa cttgacaaga gaaatgataa acatttaga acgatgtgaa    1800
catcgaatca tggaatccct tgcatggctc tcagattcac cttatttga tcttattaaa    1860
caatcaaagg accgagaagg accaactgat caccttgaat ctgcttgtcc tcttaatctt   1920
```

```
cctctccaga ataatcacac tgcagcagat atgtatcttt ctcctgtaag atctccaaag   1980
aaaaaaggtt caactacgcg tgtaaattct actgcaaatg cagagacaca agcaacctca   2040
gccttccaga cccagaagcc attgaaatct acctctcttt cactgtttta taaaaaagtg   2100
tatcggctag cctatctccg gctaaataca ctttgtgaac gccttctgtc tgagcaccca   2160
gaattagaac atatcatctg gacccttttc cagcacaccc tgcagaatga gtatgaactc   2220
atgagagaca ggcatttgga ccaaattatg atgtgttcca tgtatggcat atgcaaagtg   2280
aagaatatag accttaaatt caaaatcatt gtaacagcat acaaggatct tcctcatgct   2340
gttcaggaga cattcaaacg tgttttgatc aaagaagagg agtatgattc tattatagta   2400
ttctataact cggtcttcat gcagagactg aaaacaaata ttttgcagta tgcttccacc   2460
aggcccccta ccttgtcacc aatacctcac attcctcgaa gcccttacaa gtttcctagt   2520
tcacccttac ggattcctgg agggaacatc tatatttcac ccctgaagag tccatataaa   2580
atttcagaag gtctgccaac accaacaaaa atgactccaa gatcaagaat cttagtatca   2640
attggtgaat cattcgggac ttctgagaag ttccagaaaa taaatcagat ggtatgtaac   2700
agcgaccgtg tgctcaaaag aagtgctgaa ggaagcaacc ctcctaaacc actgaaaaaa   2760
ctacgctttg atattgaagg atcagatgaa gcagatggaa gtaaacatct cccaggagag   2820
tccaaatttc agcagaaact ggcagaaatg acttctactc gaacacgaat gcaaaagcag   2880
aaaatgaatg atagcatgga tacctcaaac aaggaagaga aatgaggatc tcaggacctt   2940
ggtggacact gtgtacacct ctggattcat tgtctctcac agatgtgact gtat        2994
```

<210> 44
<211> 782
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 44
```
Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
1               5                   10                  15
Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
                20                  25                  30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
            35                  40                  45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
        50                  55                  60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
65                  70                  75                  80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
                85                  90                  95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
                100                 105                 110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
            115                 120                 125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
        130                 135                 140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145                 150                 155                 160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
                165                 170                 175
Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
                180                 185                 190
Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
            195                 200                 205
Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
        210                 215                 220
His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225                 230                 235                 240
```

```
Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
                245             250             255
Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln
            260             265             270
Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
            275             280             285
Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
    290             295             300
Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro
305             310             315             320
Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
            325             330             335
Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr
            340             345             350
Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
            355             360             365
Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly
    370             375             380
Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp
385             390             395             400
Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
            405             410             415
Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala
            420             425             430
Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
            435             440             445
Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
    450             455             460
Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
465             470             475             480
Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
            485             490             495
Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
            500             505             510
Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
            515             520             525
Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
    530             535             540
Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro
545             550             555             560
Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr
            565             570             575
Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
            580             585             590
Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
            595             600             605
Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
    610             615             620
Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
625             630             635             640
Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
            645             650             655
Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
            660             665             670
Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
            675             680             685
Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
    690             695             700
Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys
705             710             715             720
```

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```
Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
              725             730             735
Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
          740             745             750
Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
          755             760             765
Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
    770             775             780
```

<210> 45
<211> 2663
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 45
```
ccaccatggc tccgcaccgc cccgcgcccg cgctgctttg cgcgctgtcc ctggcgctgt      60
gcgcgctgtc gctgcccgtc cgcgcggcca ctgcgtcgcg gggggcgtcc caggcggggg     120
cgccccaggg gcgggtgccc gaggcgcggc ccaacagcat ggtggtggaa caccccgagt     180
tcctcaaggc agggaaggag cctggcctgc agatctggcg tgtggagaag ttcgatctgg     240
tgcccgtgcc caccaacctt tatggagact tcttcacggg cgacgcctac gtcatcctga     300
agacagtgca gctgaggaac ggaaatctgc agtatgacct ccactactgg ctgggcaatg     360
agtgcagcca ggatgagagc ggggcggccg ccatctttac cgtgcagctg gatgactacc     420
tgaacggccg ggccgtgcag caccgtgagg tccagggctt cgagtcggcc accttcctag     480
gctacttcaa gtctggcctg aagtacaaga aaggaggtgt ggcatcagga ttcaagcacg     540
tggtacccaa cgaggtggtg gtgcagagac tcttccaggt caaagggcgg cgtgtggtcc     600
gtgccaccga ggtacctgtg tcctgggaga gcttcaacaa tggcgactgc ttcatcctgg     660
acctgggcaa caacatccac cagtggtgtg gttccaacag caatcggtat gaaagactga     720
aggccacaca ggtgtccaag ggcatccggg acaacgagcg gagtggccgg ccccgagtgc     780
acgtgtctga ggagggcact gagcccgagg cgatgctcca ggtgctgggc cccaagccgg     840
ctctgcctgc aggtaccgag gacaccgcca aggaggatgc ggccaaccgc aagctggcca     900
agctctacaa ggtctccaat ggtgcaggga ccatgtccgt ctccctcgtg gctgatgaga     960
accccttcgc ccagggggcc ctgaagtcag aggactgctt catcctggac cacggcaaag    1020
atgggaaaat ctttgtctgg aaaggcaagc aggcaaacac ggaggagagg aaggctgccc    1080
tcaaaacagc ctctgacttc atcaccaaga tggactaccc caagcagact caggtctcgg    1140
tccttcctga gggcggtgag accccactgt tcaagcagtt cttcaagaac tggcgggacc    1200
cagaccagac agatggcctg ggcttgtcct acctttccag ccatatcgcc aacgtggagc    1260
gggtgccctt cgacgccgcc accctgcaca cctccactgc catggccgcc cagcacggca    1320
tggatgacga tggcacaggc cagaaacaga tctggagaat cgaaggttcc aacaaggtgc    1380
ccgtggaccc tgccacatat ggacagttct atggaggcga cagctacatc attctgtaca    1440
actaccgcca tggtggccgc caggggcaga taatctataa ctggcagggt gcccagtcta    1500
cccaggatga ggtcgctgca tctgccatcc tgactgctca gctggatgag gagctgggag    1560
gtacccctgt ccagagccgt gtggtccaag gcaaggagcc cgcccacctc atgagcctgt    1620
ttggtgggaa gcccatgatc atctacaagg gcggcacctc ccgcgagggc gggcagacag    1680
cccctgccag cacccgcctc ttccaggtcc gcgccaacag cgctggagcc acccgggctg    1740
ttgaggtatt gcctaaggct ggtgcactga actccaacga tgcctttgtt ctgaaaaccc    1800
cctcagccgc ctacctgtgg gtgggtacag gagccagcga ggcagagaag acggggggccc    1860
aggagctgct cagggtgctg cgggcccaac ctgtgcaggt ggcagaaggc agcgagccag    1920
atggcttctg ggaggccctg ggcgggaagg ctgcctaccg cacatcccca cggctgaagg    1980
acaagaagat ggatgcccat cctcctcgcc tctttgcctg ctccaacaag attggacgtt    2040
ttgtgatcga gaggttcct ggtgagctca tgcaggaaga cctggcaacg gatgacgtca    2100
tgcttctgga cacctgggac caggtctttg tctgggttgg aaaggattct caagaagaag    2160
aaaagacaga agccttgact tctgctaagc ggtacatcga gacggaccca gccaatcggg    2220
atcggcggac gcccatcacc gtggtgaagc aaggctttga gcctccctcc tttgtgggct    2280
ggttccttgg ctgggatgat gattactggt ctgtggaccc cttggacagg gccatggctg    2340
agctggctgc ctgaggaggg gcagggccca cccatgtcac cggtcagtgc cttttggaac    2400
tgtccttccc tcaaagaggc cttagagcga gcagagcagc tctgctatga gtgtgtgtgt    2460
gtgtgtgtgt tgtttctttt tttttttttt acagtatcca aaaatagccc tgcaaaaatt    2520
```

cagagtcctt gcaaaattgt ctaaaatgtc agtgtttggg aaattaaatc caataaaaac   2580

attttgaagt gtgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   2640
aaaaaaaaaa aaaaaaaaaa aaa   2663

<210> 46
<211> 1441
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 46
Met Ser Gly Leu Gly Asp Ser Ser Ser Asp Pro Ala Asn Pro Asp Ser
 1   5   10   15
His Lys Arg Lys Gly Ser Pro Cys Asp Thr Leu Ala Ser Ser Thr Glu
            20   25   30
Lys Arg Arg Arg Glu Gln Glu Asn Lys Tyr Leu Glu Glu Leu Ala Glu
            35   40   45
Leu Leu Ser Ala Asn Ile Ser Asp Ile Asp Ser Leu Ser Val Lys Pro
    50   55   60
Asp Lys Cys Lys Ile Leu Lys Lys Thr Val Asp Gln Ile Gln Leu Met
65   70   75   80
Lys Arg Met Glu Gln Glu Lys Ser Thr Thr Asp Asp Asp Val Gln Lys
            85   90   95
Ser Asp Ile Ser Ser Ser Ser Gln Gly Val Ile Glu Lys Glu Ser Leu
            100   105   110
Gly Pro Leu Leu Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn
    115   120   125
Cys Glu Gly Arg Ile Val Phe Val Ser Glu Asn Val Thr Ser Tyr Leu
    130   135   140
Gly Tyr Asn Gln Glu Glu Leu Met Asn Thr Ser Val Tyr Ser Ile Leu
145   150   155   160
His Val Gly Asp His Ala Glu Phe Val Lys Asn Leu Leu Pro Lys Ser
            165   170   175
Leu Val Asn Gly Val Pro Trp Pro Gln Glu Ala Thr Arg Arg Asn Ser
            180   185   190
His Thr Phe Asn Cys Arg Met Leu Ile His Pro Pro Asp Glu Pro Gly
            195   200   205
Thr Glu Asn Gln Glu Ala Cys Gln Arg Tyr Glu Val Met Gln Cys Phe
    210   215   220
Thr Val Ser Gln Pro Lys Ser Ile Gln Glu Asp Gly Glu Asp Phe Gln
225   230   235   240
Ser Cys Leu Ile Cys Ile Ala Arg Arg Leu Pro Arg Pro Pro Ala Ile
            245   250   255
Thr Gly Val Glu Ser Phe Met Thr Lys Gln Asp Thr Thr Gly Lys Ile
            260   265   270
Ile Ser Ile Asp Thr Ser Ser Leu Arg Ala Ala Gly Arg Thr Gly Trp
            275   280   285
Glu Asp Leu Val Arg Lys Cys Ile Tyr Ala Phe Phe Gln Pro Gln Gly
    290   295   300
Arg Glu Pro Ser Tyr Ala Arg Gln Leu Phe Gln Glu Val Met Thr Arg
305   310   315   320
Gly Thr Ala Ser Ser Pro Ser Tyr Arg Phe Ile Leu Asn Asp Gly Thr
            325   330   335
Met Leu Ser Ala His Thr Lys Cys Lys Leu Cys Tyr Pro Gln Ser Pro
            340   345   350
Asp Met Gln Pro Phe Ile Met Gly Ile His Ile Ile Asp Arg Glu His
            355   360   365

```
Ser Gly Leu Ser Pro Gln Asp Asp Thr Asn Ser Gly Met Ser Ile Pro
    370             375             380
Arg Val Asn Pro Ser Val Asn Pro Ser Ile Ser Pro Ala His Gly Val
385             390             395                     400
Ala Arg Ser Ser Thr Leu Pro Pro Ser Asn Ser Asn Met Val Ser Thr
            405             410                     415
Arg Ile Asn Arg Gln Gln Ser Ser Asp Leu His Ser Ser Ser His Ser
            420             425                     430
Asn Ser Ser Asn Ser Gln Gly Ser Phe Gly Cys Ser Pro Gly Ser Gln
        435             440             445
Ile Val Ala Asn Val Ala Leu Asn Lys Gly Gln Ala Ser Ser Gln Ser
    450             455             460
Ser Lys Pro Ser Leu Asn Leu Asn Asn Pro Pro Met Glu Gly Thr Gly
465             470             475                     480
Ile Ser Leu Ala Gln Phe Met Ser Pro Arg Arg Gln Val Thr Ser Gly
            485             490                     495
Leu Ala Thr Arg Pro Arg Met Pro Asn Asn Ser Phe Pro Pro Asn Ile
            500             505             510
Ser Thr Leu Ser Ser Pro Val Gly Met Thr Ser Ser Ala Cys Asn Asn
            515             520             525
Asn Asn Arg Ser Tyr Ser Asn Ile Pro Val Thr Ser Leu Gln Gly Met
    530             535             540
Asn Glu Gly Pro Asn Asn Ser Val Gly Phe Ser Ala Ser Ser Pro Val
545             550             555                     560
Leu Arg Gln Met Ser Ser Gln Asn Ser Pro Ser Arg Leu Asn Ile Gln
            565             570             575
Pro Ala Lys Ala Glu Ser Lys Asp Asn Lys Glu Ile Ala Ser Thr Leu
            580             585             590
Asn Glu Met Ile Gln Ser Asp Asn Ser Ser Ser Asp Gly Lys Pro Leu
            595             600             605
Asp Ser Gly Leu Leu His Asn Asn Asp Arg Leu Ser Asp Gly Asp Ser
    610             615             620
Lys Tyr Ser Gln Thr Ser His Lys Leu Val Gln Leu Leu Thr Thr Thr

625             630             635                     640
Ala Glu Gln Gln Leu Arg His Ala Asp Ile Asp Thr Ser Cys Lys Asp
            645             650             655
Val Leu Ser Cys Thr Gly Thr Ser Asn Ser Ala Ser Ala Asn Ser Ser

            660             665             670
Gly Gly Ser Cys Pro Ser Ser His Ser Ser Leu Thr Ala Arg His Lys
            675             680             685
Ile Leu His Arg Leu Leu Gln Glu Gly Ser Pro Ser Asp Ile Thr Thr
    690             695             700
Leu Ser Val Glu Pro Asp Lys Lys Asp Ser Ala Ser Thr Ser Val Ser
705             710             715                     720
Val Thr Gly Gln Val Gln Gly Asn Ser Ser Ile Lys Leu Glu Leu Asp
            725             730             735
Ala Ser Lys Lys Lys Glu Ser Lys Asp His Gln Leu Leu Arg Tyr Leu
            740             745             750
Leu Asp Lys Asp Glu Lys Asp Leu Arg Ser Thr Pro Asn Leu Ser Leu
            755             760             765
Asp Asp Val Lys Val Lys Val Glu Lys Lys Glu Gln Met Asp Pro Cys
    770             775             780
Asn Thr Asn Pro Thr Pro Met Thr Lys Pro Thr Pro Glu Glu Ile Lys
785             790             795                     800
Leu Glu Ala Gln Ser Gln Phe Thr Ala Asp Leu Asp Gln Phe Asp Gln
            805             810             815
Leu Leu Pro Thr Leu Glu Lys Ala Ala Gln Leu Pro Gly Leu Cys Glu
            820             825             830
```

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Thr Asp Arg Met Asp Gly Ala Val Thr Ser Val Thr Ile Lys Ser Glu
        835             840             845
Ile Leu Pro Ala Ser Leu Gln Ser Ala Thr Ala Arg Pro Thr Ser Arg
        850             855             860
Leu Asn Arg Leu Pro Glu Leu Glu Leu Glu Ala Ile Asp Asn Gln Phe
865             870             875             880
Gly Gln Pro Gly Thr Gly Asp Gln Ile Pro Trp Thr Asn Asn Thr Val
        885             890             895
Thr Ala Ile Asn Gln Ser Lys Ser Glu Asp Gln Cys Ile Ser Ser Gln
        900             905             910
Leu Asp Glu Leu Leu Cys Pro Pro Thr Thr Val Glu Gly Arg Asn Asp
        915             920             925
Glu Lys Ala Leu Leu Glu Gln Leu Val Ser Phe Leu Ser Gly Lys Asp
        930             935             940
Glu Thr Glu Leu Ala Glu Leu Asp Arg Ala Leu Gly Ile Asp Lys Leu
945             950             955             960
Val Gln Gly Gly Gly Leu Asp Val Leu Ser Glu Arg Phe Pro Pro Gln
        965             970             975
Gln Ala Thr Pro Pro Leu Ile Met Glu Glu Arg Pro Asn Leu Tyr Ser
        980             985             990
Gln Pro Tyr Ser Ser Pro Phe Pro Thr Ala Asn Leu Pro Ser Pro Phe
        995             1000            1005
Gln Gly Met Val Arg Gln Lys Pro Ser Leu Gly Thr Met Pro Val Gln
        1010            1015            1020
Val Thr Pro Pro Arg Gly Ala Phe Ser Pro Gly Met Gly Met Gln Pro
1025            1030            1035            1040
Arg Gln Thr Leu Asn Arg Pro Pro Ala Ala Pro Asn Gln Leu Arg Leu
        1045            1050            1055
Gln Leu Gln Gln Arg Leu Gln Gly Gln Gln Gln Leu Ile His Gln Asn
        1060            1065            1070
Arg Gln Ala Ile Leu Asn Gln Phe Ala Ala Thr Ala Pro Val Gly Ile
        1075            1080            1085
Asn Met Arg Ser Gly Met Gln Gln Gln Ile Thr Pro Gln Pro Pro Leu
        1090            1095            1100
Asn Ala Gln Met Leu Ala Gln Arg Gln Arg Glu Leu Tyr Ser Gln Gln
1105            1110            1115            1120
His Arg Gln Arg Gln Leu Ile Gln Gln Gln Arg Ala Met Leu Met Arg
        1125            1130            1135
Gln Gln Ser Phe Gly Asn Asn Leu Pro Pro Ser Ser Gly Leu Pro Val
        1140            1145            1150
Gln Thr Gly Asn Pro Arg Leu Pro Gln Gly Ala Pro Gln Gln Phe Pro
        1155            1160            1165
Tyr Pro Pro Asn Tyr Gly Thr Asn Pro Gly Thr Pro Pro Ala Ser Thr
        1170            1175            1180
Ser Pro Phe Ser Gln Leu Ala Ala Asn Pro Glu Ala Ser Leu Ala Asn
1185            1190            1195            1200
Arg Asn Ser Met Val Ser Arg Gly Met Thr Gly Asn Ile Gly Gly Gln
        1205            1210            1215
Phe Gly Thr Gly Ile Asn Pro Gln Met Gln Gln Asn Val Phe Gln Tyr
        1220            1225            1230
Pro Gly Ala Gly Met Val Pro Gln Gly Glu Ala Asn Phe Ala Pro Ser
        1235            1240            1245
Leu Ser Pro Gly Ser Ser Met Val Pro Met Pro Ile Pro Pro Pro Gln
        1250            1255            1260
Ser Ser Leu Leu Gln Gln Thr Pro Pro Ala Ser Gly Tyr Gln Ser Pro
1265            1270            1275            1280
Asp Met Lys Ala Trp Gln Gln Gly Ala Ile Gly Asn Asn Asn Val Phe
        1285            1290            1295
Ser Gln Ala Val Gln Asn Gln Pro Thr Pro Ala Gln Pro Gly Val Tyr
        1300            1305            1310
```

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Asn Asn Met Ser Ile Thr Val Ser Met Ala Gly Gly Asn Thr Asn Val
        1315                1320                1325
Gln Asn Met Asn Pro Met Met Ala Gln Met Gln Met Ser Ser Leu Gln
    1330                1335                1340
Met Pro Gly Met Asn Thr Val Cys Pro Glu Gln Ile Asn Asp Pro Ala
1345                1350                1355                1360
Leu Arg His Thr Gly Leu Tyr Cys Asn Gln Leu Ser Ser Thr Asp Leu
                1365                1370                1375
Leu Lys Thr Glu Ala Asp Gly Thr Gln Gln Val Gln Gln Val Gln Val
            1380                1385                1390
Phe Ala Asp Val Gln Cys Thr Val Asn Leu Val Gly Gly Asp Pro Tyr
        1395                1400                1405
Leu Asn Gln Pro Gly Pro Leu Gly Thr Gln Lys Pro Thr Ser Gly Pro
    1410                1415                1420
Gln Thr Pro Gln Ala Gln Gln Lys Ser Leu Arg Gln Gln Leu Leu Thr
1425                1430                1435                1440
Glu
```

```
<210> 47
<211> 4547
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
      synthetic construct

<400> 47
cggatccact agtccagtgt ggtggaattc ggcttcatca tcatgagtgg ccttggggac    60
agttcatccg accctgctaa cccagactca cataagagga aaggatcgcc atgtgacaca   120
ctggcatcaa gcacggaaaa gaggcgcagg gagcaagaaa ataaatattt agaagaacta   180
gctgagttac tgtctgccaa cattagtgac attgacagct tgagtgtaaa accagacaaa   240
tgcaagattt tgaagaaaac agtcgatcag atacagctaa tgaagagaat ggaacaagag   300
aaatcaacaa ctgatgacga tgtacagaaa tcagacatct catcaagtag tcaaggagtg   360
atagaaaagg aatccttggg acctcttctt ttggaggctt tggatggatt tttctttgtt   420
gtgaactgtg aagggagaat tgtatttgtg tcagagaatg taaccagcta cttaggttac   480
aatcaggagg aattaatgaa tacgagcgtc tacagcatac tgcacgtggg ggatcatgca   540
gaatttgtga agaatctgct accaaaatca ctagtaaatg gagttccttg cctcaagag    600
gcaacacgac gaaatagcca tacctttaac tgcaggatgc taattcaccc tccagatgag   660
ccagggaccg agaaccaaga agcttgccag cgttatgaag taatgcagtg tttcactgtg   720
tcacagccaa aatcaattca agaggatgga gaagatttcc agtcatgtct gatttgtatt   780
gcacggcgat tacctcggcc tccagctatt acgggtgtag aatcctttat gaccaagcaa   840
gatactacag gtaaaatcat ctctattgat actagttccc tgagagctgc tggcagaact   900
ggttgggaag atttagtgag gaagtgcatt tatgcttttt tccaacctca gggcagagaa   960
ccatcttatg ccagacagct gttccaagaa gtgatgactc gtggcactgc ctccagcccc  1020
tcctatagat tcatattgaa tgatgggaca atgcttagcg cccacaccaa gtgtaaactt  1080
tgctaccctc aaagtccaga catgcaacct ttcatcatgg gaattcatat catcgacagg  1140
gagcacagtg ggctttctcc tcaagatgac actaattctg gaatgtcaat tccccgagta  1200
aatccctcgg tcaatcctag tatctctcca gctcatggtg tggctcgttc atccacattg  1260

ccaccatcca acagcaacat ggtatccacc agaataaacc gccagcagag ctcagacctt  1320
catagcagca gtcatagtaa ttctagcaac agccaaggaa gtttcggatg ctcacccgga  1380
agtcagattg tagccaatgt tgccttaaac aaaggacagg ccagttcaca gagcagtaaa  1440
ccctcttaa acctcaataa tcctcctatg gaaggtacag gaatatccct agcacagttc   1500
atgtctccaa ggagacaggt tacttctgga ttggcaacaa ggcccaggat gccaaacaat  1560
tcctttcctc ctaatatttc gacattaagc tctcccgttg gcatgacaag tagtgcctgt  1620
aataataata accgatctta ttcaaacatc ccagtaacat ctttacaggg tatgaatgaa  1680
ggacccaata actccgttgg cttctctgcc agttctccag tcctcaggca gatgagctca  1740
cagaattcac ctagcagatt aaatatacaa ccagcaaaag ctgagtccaa agataacaaa  1800
gagattgcct caactttaaa tgaaatgatt caatctgaca acagctctag tgatggcaaa  1860
```

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cctctggatt cagggcttct gcataacaat gacagacttt cagatggaga cagtaaatac  1920
tctcaaacca gtcacaaact agtgcagctt ttgacaacaa ctgccgaaca gcagttacgg  1980
catgctgata tagacacaag ctgcaaagat gtcctgtctt gcacaggcac ttccaactct  2040
gcctctgcta actcttcagg aggttcttgt ccctcttctc atagctcatt gacagcacgg  2100
cataaaattc tacaccggct cttacaggag ggtagcccct cagatatcac cactttgtct  2160
gtcgagcctg ataaaaagga cagtgcatct acttctgtgt cagtgactgg acaggtacaa  2220
ggaaactcca gtataaaact agaactggat gcttcaaaga aaaaagaatc aaaagaccat  2280
cagctcctac gctatctttt agataaagat gagaaagatt taagatcaac tccaaacctg  2340
agcctggatg atgtaaaggt gaaagtggaa aagaaagaac agatggatcc atgtaataca  2400
aacccaaccc caatgaccaa acccactcct gaggaaataa aactggaggc ccagagccag  2460
tttacagctg accttgacca gtttgatcag ttactgccca cgctggagaa ggcagcacag  2520
ttgccaggct tatgtgagac agacaggatg gatggtgcgg tcaccagtgt aaccatcaaa  2580
tcggagatcc tgccagcttc acttcagtcc gccactgcca gacccacttc caggctgaat  2640
agattacctg agctggaatt ggaagcaatt gataaccaat ttggacaacc aggaacaggc  2700
gatcagattc catggacaaa taatacagtg acagctataa atcagagtaa atcagaagac  2760
cagtgtatta gctcacaatt agatgagctt ctctgtccac ccacaacagt agaagggaga  2820
aatgatgaga aggctcttct tgaacagctg gtatccttcc ttagtggcaa agatgaaact  2880
gagctagctg aactagacag agctctggga attgacaaac ttgttcaggg gggtggatta  2940
gatgtattat cagagagatt tccaccacaa caagcaacgc cacctttgat catggaagaa  3000
agacccaacc tttattccca gccttactct tctccttttc ctactgccaa tctccctagc  3060
cctttccaag gcatggtcag gcaaaaacct tcactgggga cgatgcctgt tcaagtaaca  3120
cctccccgag gtgctttttc acctggcatg ggcatgcagc ccaggcaaac tctaaacaga  3180
cctccggctg cacctaacca gcttcgactt caactacagc agcgattaca gggacaacag  3240
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